

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 11:25:55 ; Search time 1696.36 Seconds  
(without alignments)  
95.477 Million cell updates/sec

Title: US-09-400-322-1  
Perfect score: 12  
Sequence: 1 gggagcttccc 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	125	9	AV744760 AV744760
2	12	100.0	135	9	AM168558 x189a04.x
3	12	100.0	139	12	AZ727644 RCCT-24-1
4	12	100.0	144	10	BF757323 MFO-CT045
5	12	100.0	178	9	AA887620 ng96a01.s
6	12	100.0	183	10	BE666630 150209 MA
7	12	100.0	183	10	BE667317 151609 MA
8	12	100.0	186	12	BH218996 1006083FI
9	12	100.0	187	9	AA917080 o147907.s
10	12	100.0	190	9	AM703817 SK13b08.Y
11	12	100.0	191	9	BE083238 RC3-EP064
12	12	100.0	191	9	AA613566 ng22f06.s
13	12	100.0	192	9	AM873686 hq28e02.x
14	12	100.0	198	9	AV357824 AV357824
15	12	100.0	201	9	AI382447 ta72e07.x
16	12	100.0	204	10	BF154634 RC2-BN040
17	12	100.0	205	10	D77250 MUSA0A05 mo

18	12	100.0	209	9	AA373341 EST85505
19	12	100.0	218	9	AM084153 xc48a07.x
20	12	100.0	222	9	AA593275 nm08d10.s
21	12	100.0	223	9	BB015270 BB015270
22	12	100.0	224	9	BB062601 BB062601
23	12	100.0	226	9	BB468472 BB468472
24	12	100.0	229	9	AI649331 uk26d07.x
25	12	100.0	232	9	BB015909 BB015909
26	12	100.0	234	12	AZ060612 RCCT-23-4
27	12	100.0	237	9	AM703816 SK13b07.Y
28	12	100.0	237	9	BB512831 BB512831
29	12	100.0	237	9	BB604122 BB604122
30	12	100.0	239	9	AV646685 AV646685
31	12	100.0	239	9	AM836013 PMO-LT001
32	12	100.0	243	9	AA578485 n16e07.s
33	12	100.0	246	12	AZ062841 RCCT-23-4
34	12	100.0	247	9	BB606343 BB606343
35	12	100.0	248	9	AA963640 UI-R-EI-9
36	12	100.0	248	9	AV277719 AV277719
37	12	100.0	249	9	AA569798 nm41f11.s
38	12	100.0	250	9	A1538725 tp57f07.x
39	12	100.0	250	9	AA344448 EST50340
40	12	100.0	251	9	AA534853 UI-R-B50-
41	12	100.0	251	9	BB289766 BB289766
42	12	100.0	252	9	BB387551 BB387551
43	12	100.0	253	9	BB010631 BB010631
44	12	100.0	254	9	A1594640 vt51b03.x
45	12	100.0	254	9	BB282512 BB282512

## ALIGNMENTS

RESULT 1  
AV744760  
LOCUS AV744760 CB Homo sapiens CDNA clone CB06JG08 5', mRNA sequence.  
DEFINITION AV744760  
ACCESSION AV744760  
VERSION AV744760.1 GI:10862341  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 125)  
Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,  
Chen, S., Mao, M. and Chen, Z.  
Homo sapiens CB library CDNA clones  
Unpublished (2000)  
Contact: Zhu Chen  
Shanghai Institute of Hematology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: mbsl@ems.stn.sh.cn

TITLE  
JOURNAL  
COMMENT  
This clone is available at Shanghai Hematology Institute in  
Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers  
1. 125

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CB06JG08"  
/clone\_id="CB"  
/tissue\_type="cord blood"  
/cell\_type="CD34+ hematopoietic stem/progenitor cell"  
/lab\_host="BM25.8"  
/note="Vector: pBluescript; Site: 1; EcoRI; The insert is  
cloned randomly with the EcoRI digestion"

BASE COUNT  
ORIGIN  
17 a 30 c 37 t 2 others

Query Match 100.0%; Score 12; DB 9; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttcgcc 12  
 |||  
 DB 45 GGGGACTTCC 56

## RESULT 2

AM168558 135 bp mRNA linear EST 12-NOV-1999  
 DEFINITION x189a04.x1 NCI-CGAP\_Mel3 Homo sapiens cDNA clone IMAGE:2652942.3',  
 mRNA sequence.

AM168558  
 AM168558.1 GI:6400083  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

## JOURNAL

CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

## COMMENT

Tissue Procurement: Robert Sikorski, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found

Seq primer: -40UP from Gibco.

## FEATURES

Location/Qualifiers

1..135  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:2652942"  
 /clone\_lib="NCI-CGAP\_Mel3"  
 /tissue\_type="metastatic melanoma to bowel"  
 /lab\_host="DH10B"  
 /note="Organ: bowel (skin primary); Vector: pCMV-SPORT4;  
 Site\_1: Salt; Site\_2: NotI; Cloned unidirectionally.  
 Primer: Oligo dT. Average insert size 0.9 kb. Life  
 Technologies catalog #: 10981-017"  
 BASE COUNT 21 a 58 c 26 g 30 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttcgcc 12  
 |||  
 DB 27 GGGGACTTCC 38

## RESULT 3

A2727644 139 bp DNA linear GSS 25-JAN-2001  
 DEFINITION RPCI-24-113M16.TV RPCI-24 Mus musculus genomic clone RPCI-24-113M16  
 , DNA sequence.

A2727644  
 A2727644.1 GI:12485140  
 GSS.

## SOURCE

house mouse.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
 AUTHORS 1 (bases 1 to 139)  
 Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akınret,B., Levins,M.,  
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,E.,  
 Russell,D., de Jong,P. and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPCI-24  
 Unpublished (1999)

## JOURNAL

Other\_GSSs: RPCI-24-113M16.TJ

## COMMENT

Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-24. For BAC  
 library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC  
 Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end  
 page: [http://www.tigr.org/cdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 113 row: M column: 16  
 Seq primer: 17  
 Class: BAC ends.

## FEATURES

source

Location/Qualifiers

1..139  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="RPCI-24-113M16"  
 /clone\_lib="RPCI-24"  
 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /note="Vector: pPRBAC1; Site\_1: BamHI; Site\_2: BamHI;  
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
 library was cloned in the pPRBAC1 cloning vector at the  
 BamHI sites using MboI partially digested male C57BL/6J  
 DNA."  
 BASE COUNT 38 a 31 c 34 g 36 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 12; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttcgcc 12  
 |||  
 DB 120 GGGGACTTCC 131

## RESULT 4

BF757323 144 bp mRNA linear EST 12-JAN-2001  
 LOCUS MRO-CT0452-041100-303-a05 CT0452 Homo sapiens cDNA, mRNA sequence.

BF757323  
 BF757323.1 GI:12105223  
 EST.

## KEYWORDS

human.

## SOURCE

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 144)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.G.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

20202663

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR06t2-MR0-C10452-  
041100-303-a036t3-2000-11-04&tl=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 143.  
Location/Qualifiers  
1. 144

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0452"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site:1: Sma1; Site:2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 32 a 28 c 53 g 30 t 1 others  
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 144;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
78 GGGGACTTCCC 67

RESULT 5  
AA887620 178 bp mRNA linear EST 07-APR-1998  
LOCUS  
DEFINITION ng96a01.s1 NCI-CGAP\_CO10 Homo sapiens cDNA IMAGE:1160136 3',  
mRNA sequence.  
ACCESSION AA887620  
-VERSION AA887620.1 GI:3003295  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 178)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.lnl.gov/bdrr/image/image.html  
Insert Length: 886 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 169.  
Location/Qualifiers  
1. 178

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1160136"

/clone\_lib="NCI-CGAP\_CO10"  
/tissue\_type="colon tumor RER+"  
/lab\_host="DH108"  
/note="Organ: colon; Vector: pT733D-Pac (Pharmacia) with a  
modified polylinker; 1st strand cDNA was prepared from  
RER+ colon tumor, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT733  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo (N-Soares4)."  
BASE COUNT 50 a 51 c 38 g 39 t  
ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 178;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
68 GGGGACTTCCC 79

RESULT 6  
BE666630/c 183 bp mRNA linear EST 25-APR-2001  
LOCUS  
DEFINITION 150209 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE666630  
VERSION BE666630.1 GI:10027221  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 183)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Wckow,C.G.,  
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
Keefe,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
21180013  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemai@marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 62 Row: M Column: 15  
Seq primer: ATTATGGGACACTATAG.  
Location/Qualifiers  
1. 183

FEATURES  
source  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 4BOV"  
/tissue\_type="pooled"  
/lab\_host="DH108"  
/note="Vector: pCMV SPORT6; Site:1: XbaI; Site:2: XhoI;  
Library made from pooled tissue from day 20 and day 40  
embryos."  
BASE COUNT 49 a 44 c 57 g 33 t  
ORIGIN

49 a 44 c 57 g 33 t

Query Match 100.0%; Score 12; DB 10; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
 |||||||  
 Db 141 GGGGACTTTCCC 130

RESULT 7  
 BE667317/c 183 bp mRNA linear EST 25-APR-2001  
 LOCUS BE667317  
 DEFINITION 151609 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BE667317  
 VERSION BE667317.1 GI:10027908  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE  
 JOURNAL Sequence evaluation of four pooled tissue normalized bovine cDNA  
 MEDLINE libraries and construction of a gene index for cattle  
 COMMENT Genome Res. 11 (4), 626-630 (2001)  
 21180013

USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smitht@mail.marc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross\_match with the -mismatch 18 and -mismatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 63 row: M column: 15  
 Seq primer: ATTAGTGACACTATAG.  
 Location/Qualifiers  
 1..183  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="MARC 4BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI; Library made from pooled tissue from day 20 and day 40 embryos."

BASE COUNT 49 a 44 c 57 g 33 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
 |||||||  
 Db 141 GGGGACTTTCCC 130

RESULT 8  
 BH218996 186 bp DNA linear GSS 08-NOV-2001  
 LOCUS BH218996  
 DEFINITION 1006083F11.x1 1006 - Rescuenmu Grid G Zea mays genomic, DNA

ACCESSION  
 VERSION BH218996.1 GI:16812479  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 186)  
 Title: Zea mays genomic sequences found using engineered Rescuenmu transposon  
 JOURNAL Walbot, V.  
 COMMENT Unpublished (2001)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.  
 Post-ligation sequence submitted separately.  
 Plate: 1006083 row: 33  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..186

FEATURES  
 source

/organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1006 - Rescuenmu Grid G"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: Rescuenmu (engineered from Bluescript backbone); Site\_1: BamHI; Site\_2: BglII; Rescuenmu is a 4.9 kb modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuenmu, go to the web site 'www.emdb.iastate.edu' and follow the links for 'Rescuenmu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 39 a 68 c 40 g 39 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 12; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
 |||||||  
 Db 104 GGGGACTTTCCC 115

RESULT 9  
 AA917080 187 bp mRNA linear EST 26-AUG-1998  
 LOCUS AA917080  
 DEFINITION O147907.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1526652 3' similar to SW:LAFF4\_HUMAN P51826 LAF-4 PROTEIN ; mRNA sequence.  
 ACCESSION AA917080  
 VERSION AA917080.1 GI:3056472  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 187)  
 REFERENCE NCI-Cgap http://www.ncbi.nlm.nih.gov/ncicgap.

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Email: cgaps-remail.nih.gov  
 Contact: Robert Strausberg, Ph.D.  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert length: 1563 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 1.  
**FEATURES**  
 source  
 1. 187  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="1526652"  
 /clone\_id="Soares\_NFL\_T\_GBC\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: p1773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell M1\_CGAP\_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

**BASE COUNT**  
 ORIGIN  
 41 a 46 c 47 g 52 t 1 others

**Query Match**  
 Best Local Similarity 100.0%; Score 12; DB 9; Length 187;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 gggagacttccc 12  
 |||||  
 Db 83 GGGGACTTTCCC 94

**RESULT 10**  
**LOCUS** .AM703817/c  
**DEFINITION** sK13P08.v1 Gm-cl023 glycine max cDNA clone GENOME SYSTEMS CLONE ID: AM703817  
**ACCESSION** Gm-cl023-3952 5', mRNA sequence.  
**VERSION** AM703817  
**KEYWORDS** EST.  
**SOURCE** soybean.  
**ORGANISM** Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 1 (bases 1 to 190)  
**REFERENCE**  
**AUTHORS** Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
**TITLE** Public Soybean EST Project  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Shoemaker R./Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

**FEATURES**  
 source  
 1. 190  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone\_image="GENOME SYSTEMS CLONE ID: Gm-cl023-3952"  
 /clone\_id="Gm-cl023"  
 /library\_type="seed coats of greenhouse grown plants"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mg) of greenhouse grown plants. The library was prepared using the Life Technologies Superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linkers adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

**BASE COUNT**  
 ORIGIN  
 58 a 35 c 51 g 46 t

**Query Match**  
 Best Local Similarity 100.0%; Score 12; DB 9; Length 190;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 gggagacttccc 12  
 |||||  
 Db 156 GGGGACTTTCCC 145

**RESULT 11**  
**LOCUS** BE083238/c  
**DEFINITION** RC3-BR0643-290200-011-d08 BT0643 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BE083238  
**VERSION** BE083238.1 GI:8473557  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 191)  
**REFERENCE**  
**AUTHORS** Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bioness, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalhal, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEEDLINE** 200202653  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=62=RC3-BR0643-290200-011-d08&tl3=2000-02-29&tl4=1)

Seq primer: puc 18 forward  
High quality sequence start: 25  
High quality sequence stop: 191.  
Location/Qualifiers

# FEATURES

1..191

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="BT0643"

/dev\_stage="Adult"

/note="Organ: breast; Vector: puc18; Site.1: Sma1; Site.2: Sma1; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196

, 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

64 c 56 g 39 t

BASE COUNT 32 a 64 c 56 g 39 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 191;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggggacttcgcc 12

Db 38 GGGGACTTTCCC 27

## RESULT 12

AA613566/c

LOCUS ng22f06.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA clone IMAGE:1144643 3',

DEFINITION mRNA sequence.

ACCESSION AA613566

VERSION AA613566.1 GI:2464604

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bdrp/image/image.html

Insert Length: 789 Std Error: 0.00

Seq primer: -40m3 fwd. Et from Amersham

High quality sequence stop: 177.

Location/Qualifiers

1..191

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="IMAGE:1144643"

/clone\_id="NCI\_CGAP\_Co10"

/tissue\_type="colon tumor RER+"

/lab\_host="DH10B"

/note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

RER+ colon tumor, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo (N-Soares4). "

BASE COUNT 60 a 46 c 54 g 31 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 191;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggggacttcgcc 12

Db 162 GGGGACTTTCCC 151

## RESULT 13

AW873686

LOCUS hg28e02.x1 NCI\_CGAP\_Adrl Homo sapiens cDNA clone IMAGE:3120698 3',

DEFINITION mRNA sequence.

ACCESSION AW873686

VERSION AW873686.1 GI:8007739

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL, send email to:

info@image.lnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 189.

Location/Qualifiers

1..192

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="IMAGE:3120698"

/clone\_id="NCI\_CGAP\_Adrl"

/tissue\_type="neuroblastoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: PCMV-SPOrt6; Site.1:

NotI; Site.2: SalI; Cloned unidirectionally. Primer:

Oligo dT. Average insert size 1.2 kb. Library

constructed by Life Technologies. 1 others

BASE COUNT 48 a 43 c 47 g 53 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 192;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggggacttcgcc 12

Db 148 GGGGACTTTCCC 159

## RESULT 14

AV357824 198 bp mRNA linear EST 13-NOV-1999

LOCUS AV357824

DEFINITION AV357824 RIKEN full-length enriched, in vitro fertilized eggs Mus

ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AV357824			mus musculus					
AV357824.1	GI:6404826		house mouse					
			mus musculus					
			Euarctota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
			1 (bases 1 to 198)					
			Komono,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kawaga,I., Kato,C., Kawai,T., Kikuchi,N., KoJime,Y., Koya,S., Kusabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateono,M., Tomioka,N., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshida,A., Yoshino,M., Muramatsu,M., and Hayashizaki,Y.					
			RIKEN Mouse ESIS (Komono,H., et al. 1999)					
			unpublished (1999)					
			Contact: Yoshihide Hayashizaki					
			Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute					
			The Institute of Physical and Chemical Research (RIKEN)					
			1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan					
			Tel: 81-45-503-9222					
			Fax: 81-45-503-9216					
			Email: genome-res@gsc.riken.go.jp,					
			URL:http://genome.gsc.riken.go.jp/					
			Sasaki,N., Izawa,M., Watabiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.					
			Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)					
			Itoh,M., Katsunai,T., Akiyama,Y., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.					
			Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)					
			Carninci,P. and Hayashizaki,Y.					
			High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)					
			Please visit our web site ( <a href="http://genome.rtc.riken.go.jp">http://genome.rtc.riken.go.jp</a> ) for further details.					
			Location/Qualifiers					
			1. 198					
			/organism="Mus musculus"					
			/strain="C57BL/6J"					
			/db_xref="taxon:10090"					
			/clone="7420409H19"					
			/clone_lib="RIKEN full-length enriched, in vitro fertilized eggs"					
			/sex="female"					
			/tissue_type="in vitro fertilized eggs"					
			/dev_stage="egg"					
			/lab_host="DH10B"					
			/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGGATCCACAGACCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the high adapter of sequence [5' GAGGAGAGATCTCGAGTTATTAATTAATTAATCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"					

BASE COUNT	53 a	42 c	55 g	48 t
ORIGIN				
Query Match	100.0%	Score 12;	DB 9;	Length 198;
Best Local Similarity	100.0%;	Pred. No. 5.8e+03;		
Matches 12; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 ggggacattccc 12			
DB	92 GGGGACTTCC 103			
RESULT 15				
AI382447/C	201 bp	mRNA	linear	EST 18-MAR-1999
LOCUS				
DEFINITION	ta72e07.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens CDNA clone			
ACCESSION	AI382447			
VERSION	AI382447.1 GI:4195228			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 201)			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
COMMENT	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapb-remail.nih.gov			
	This clone is available royalty-free through LNL ; contact the			
	IMAGE Consortium (info@image.llnl.gov) for further information.			
	Insert Length: 473 Std Error: 0.00			
	Seq primer: -40UP from Gibco			
	High quality sequence stop: 190.			
FEATURES	Location/Qualifiers			
SOURCE	1..201			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:2049636"			
	/clone_lib="Soares_total_fetus_Nb2HF8_9w"			
	/dev_stage="8-9 weeks"			
	/lab_host="DH10B"			
	/note="Vector: p7T73D-Pac (Pharmacia) with a modified			
	polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA			
	was prepared from mRNA obtained from pooled 8-9 week			
	(total) fetus material with a Not I - oligo(dT) primer [5'			
	TGTACCAATCTGAATGGGAGCGCGCTTAATTTTTTTTTTTT 3'].			
	Double-stranded cDNA was ligated to Eco RI adaptors			
	(Pharmacia), digested with Not I and cloned into the Not I			
	and Eco RI sites of the modified p7T73 vector. Library			
	went through one round of normalization, and was			
	constructed by Bento Soares and M. Fatima Bonaldo. "			
BASE COUNT	62 a	39 c	30 g	70 t
ORIGIN				
Query Match	100.0%;	Score 12;	DB 9;	Length 201;
Best Local Similarity	100.0%;	Pred. No. 5.8e+03;		
Matches 12; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 ggggacattccc 12			
DB	71 GGGGACTTCC 60			

Search completed: September 22, 2002, 12:49:38  
Job time: 5023 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 12:21:04 : Search time 2898.72 Seconds  
(without alignments)  
89.563 Million cell updates/sec

Title: US-09-400-322-1  
Perfect score: 12  
Sequence: 1 ggggacttccc 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main.\*

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2: /cgn2_6/ptodata/1/pna/US0905B.COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US0905C.COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US0905D.COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US0905E.COMB.seq.*
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7: /cgn2_6/ptodata/1/pna/US0905G.COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US0905H.COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US0905I.COMB.seq.*
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33: /cgn2_6/ptodata/1/pna/US0906G.COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US0906H.COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US0906I.COMB.seq.*
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37: /cgn2_6/ptodata/1/pna/US0906K.COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US0906L.COMB.seq.*
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41: /cgn2_6/ptodata/1/pna/US0906O.COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US0906P.COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US0906Q.COMB.seq.*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	1	PCT-US00-00770-16
2	12	100.0	12	1	PCT-US00-00807-23
3	12	100.0	12	1	PCT-US00-00903-8
4	12	100.0	12	1	PCT-US00-01239-30
5	12	100.0	12	1	PCT-US00-03062-8
6	12	100.0	12	1	PCT-US00-03062-8
7	12	100.0	12	1	PCT-US00-04572-24
8	12	100.0	12	1	PCT-US00-05881-844
9	12	100.0	12	1	PCT-US00-05882-1692
10	12	100.0	12	1	PCT-US00-05883-1554
11	12	100.0	12	1	PCT-US00-05918-894
12	12	100.0	12	1	PCT-US00-05988-1888
13	12	100.0	12	1	PCT-US00-05989-926
14	12	100.0	12	1	PCT-US00-06012-8
15	12	100.0	12	1	PCT-US00-06013-8
16	12	100.0	12	1	PCT-US00-06014-8
17	12	100.0	12	1	PCT-US00-06043-8
18	12	100.0	12	1	PCT-US00-06049-8
19	12	100.0	12	1	PCT-US00-06057-8
20	12	100.0	12	1	PCT-US00-06059-8
21	12	100.0	12	1	PCT-US00-06765-8
22	12	100.0	12	1	PCT-US00-06765-8
23	12	100.0	12	1	PCT-US00-06781-8
24	12	100.0	12	1	PCT-US00-06782-8
25	12	100.0	12	1	PCT-US00-06783-8
26	12	100.0	12	1	PCT-US00-06791-8
27	12	100.0	12	1	PCT-US00-06792-8
28	12	100.0	12	1	PCT-US00-06792-8
29	12	100.0	12	1	PCT-US00-06822-8
30	12	100.0	12	1	PCT-US00-06823-8
31	12	100.0	12	1	PCT-US00-06824-8

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32 12 100.0 12 1 PCT-US00-06828-8 Sequence 8, Appl1
33 12 100.0 12 1 PCT-US00-06830-8 Sequence 8, Appl1
34 12 100.0 12 1 PCT-US00-07440-8 Sequence 8, Appl1
35 12 100.0 12 1 PCT-US00-07440A-8 Sequence 8, Appl1
36 12 100.0 12 1 PCT-US00-07483-8 Sequence 8, Appl1
37 12 100.0 12 1 PCT-US00-07505-8 Sequence 8, Appl1
38 12 100.0 12 1 PCT-US00-07506-8 Sequence 8, Appl1
39 12 100.0 12 1 PCT-US00-07507-8 Sequence 8, Appl1
40 12 100.0 12 1 PCT-US00-07526-8 Sequence 8, Appl1
41 12 100.0 12 1 PCT-US00-07527-8 Sequence 8, Appl1
42 12 100.0 12 1 PCT-US00-07534-8 Sequence 8, Appl1
43 12 100.0 12 1 PCT-US00-07535-8 Sequence 8, Appl1
44 12 100.0 12 1 PCT-US00-07578-8 Sequence 8, Appl1
45 12 100.0 12 1 PCT-US00-07578-8 Sequence 8, Appl1
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## ALIGNMENTS

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RESULT 1
PCT-US00-00770-16
; Sequence 16, Application PC/TUS0000770
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Bone Marrow-Specific Protein
; FILE REFERENCE: PF495.PCT
; CURRENT APPLICATION NUMBER: PCT/US00/00770
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: 60/116,236
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-00770-16
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Query Match 100.0%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 999gacttcgcc 12
Db 1 999gacttcgcc 12
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RESULT 2
PCT-US00-00807-23
; Sequence 23, Application PC/TUS0000807
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399PCT2
; CURRENT APPLICATION NUMBER: PCT/US00/00807
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 09/231,788
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 23
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-00807-23
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Query Match 100.0%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 999gacttcgcc 12
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Db 1 999gacttcgcc 12
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RESULT 3
PCT-US00-00903-8
; Sequence 8, Application PC/TUS0000903
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 33 Human Secreted Proteins
; FILE REFERENCE: P2036.PCT
; CURRENT APPLICATION NUMBER: PCT/US00/00903
; CURRENT FILING DATE: 2000-01-18
; EARLIER APPLICATION NUMBER: 60/116,330
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-00903-8
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Query Match 100.0%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 999gacttcgcc 12
Db 1 999gacttcgcc 12
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RESULT 4
PCT-US00-01239-30
; Sequence 30, Application PC/TUS0001239
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Keratinocyte Derived Interferon
; FILE REFERENCE: PF482P1
; CURRENT APPLICATION NUMBER: PCT/US00/01239
; CURRENT FILING DATE: 2000-01-20
; EARLIER APPLICATION NUMBER: 60/093,643
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: PCT/US99/16424
; EARLIER FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 30
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-01239-30
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Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 999gacttcgcc 12
Db 1 999gacttcgcc 12
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RESULT 5
PCT-US00-03062-8
; Sequence 8, Application PC/TUS0003062A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 33 Human secreted proteins
; FILE REFERENCE: P2037.PCT
; CURRENT APPLICATION NUMBER: PCT/US00/03062A
; CURRENT FILING DATE: 2000-02-08
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EARLIER APPLICATION NUMBER: 60/119,468  
EARLIER FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-03062-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||

Db 1 ggggacttccc 12

RESULT 6  
PCT-US00-03062-8  
Sequence 8, Application PC/TUS0003062B  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: 33 Human secreted proteins  
FILE REFERENCE: P2037.PCT  
CURRENT APPLICATION NUMBER: PCT/US00/03062B  
CURRENT FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/119,468  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-03062-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 7  
PCT-US00-04572-24  
Sequence 24, Application PC/TUS0004572  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins  
TITLE OF INVENTION: TR1, TR1SV1, and TR1SV2  
FILE REFERENCE: PF396.PCT2  
CURRENT APPLICATION NUMBER: PCT/US00/04572  
CURRENT FILING DATE: 2000-02-23  
EARLIER APPLICATION NUMBER: 60/121,648  
EARLIER FILING DATE: 1999-02-24  
EARLIER APPLICATION NUMBER: 60/134,172  
EARLIER FILING DATE: 1999-05-13  
EARLIER APPLICATION NUMBER: 60/144,076  
EARLIER FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 24  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-04572-24

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||

Db 1 ggggacttccc 12

RESULT 8  
PCT-US00-05881-844  
Sequence 844, Application PC/TUS0005881  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben,  
TITLE OF INVENTION: Human Breast and Ovarian Cancer Associated Gene Sequences and  
FILE REFERENCE: PA103PCT  
CURRENT APPLICATION NUMBER: PCT/US00/05881  
CURRENT FILING DATE: 2000-03-08  
EARLIER APPLICATION NUMBER: 60/124,270  
EARLIER FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 846  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 844  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-05881-844

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 9  
PCT-US00-05882-1692  
Sequence 1692, Application PC/TUS0005882  
GENERAL INFORMATION:  
APPLICANT: Steve Ruben,  
APPLICANT: Craig Rosen,  
TITLE OF INVENTION: Human Cancer Associated Gene Sequences and Polypeptides  
FILE REFERENCE: PA106PCT  
CURRENT APPLICATION NUMBER: PCT/US00/05882  
CURRENT FILING DATE: 2000-03-08  
EARLIER APPLICATION NUMBER: 60/124,270  
EARLIER FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 1692  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-05882-1692

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 10  
PCT-US00-05883-1554  
Sequence 1554, Application PC/TUS0005883

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; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Colon Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PA102PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05883
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270.
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1554
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-05883-1554

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 999gacttccc 12
Db 1 999gacttccc 12

RESULT 11
PCT-US00-05918-894
; Sequence 894, Application PC/TUS0005918
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Lung Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PA104PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05918
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 894
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-05918-894

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 999gacttccc 12
Db 1 999gacttccc 12

RESULT 12
PCT-US00-05988-1888
; Sequence 1888, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PA101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1888
; LENGTH: 12
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-05988-1888

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 999gacttccc 12
Db 1 999gacttccc 12

RESULT 13
PCT-US00-05989-926
; Sequence 926, Application PC/TUS0005989
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Pancreas and Pancreatic Cancer Associated Gene Sequences
; FILE REFERENCE: PA105PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05989
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 926
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-05989-926

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 999gacttccc 12
Db 1 999gacttccc 12

RESULT 14
PCT-US00-06012-8
; Sequence 8, Application PC/TUS0006012
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PS502PCT
; CURRENT APPLICATION NUMBER: PCT/US00/06012
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: 60/124,093
; EARLIER FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 60/166,989
; EARLIER FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-06012-8

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 999gacttccc 12
Db 1 999gacttccc 12
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Db 1 ggggacttccc 12

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RESULT 15
PCT-US00-06013-8
; Sequence 8, Application PC/TUS0006013
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PS508PCT
; CURRENT APPLICATION NUMBER: PCT/US00/06013
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: 60/125,360
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 60/138,626
; EARLIER FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 60/168,662
; EARLIER FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-06013-8
    
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Query Match 100.0%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ggggacttccc 12
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Db 1 ggggacttccc 12
    
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Search completed: September 22, 2002, 14:14:46  
 Job time: 6822 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 12:49:45 : Search time 325.71 Seconds  
(without alignments)  
118.209 Million cell updates/sec

Title: US-09-400-322-1  
Perfect score: 12  
Sequence: 1 999gacttcctccc 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2138461 seqs, 1604250230 residues

Total number of hits satisfying chosen parameters: 4276922

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	12	100.0	12 1 PCT-US02-09135-8	Sequence 8, Appli
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14	12	100.0	12 1 PCT-US02-21857-14	Sequence 14, Appli
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16	12	100.0	12 5 US-09-572-406B-26	Sequence 26, Appli
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#### ALIGNMENTS

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RESULT 1
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; Sequence 8, Application PC/TUS0201109
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/01109
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-01109-8

Query Match      100.0%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 999gacttcctccc 12
Db      1 999gacttcctccc 12

RESULT 2
PCT-US02-06990-8
; Sequence 8, Application PC/TUS0206990
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PF534PCT
; CURRENT APPLICATION NUMBER: PCT/US02/06990
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,214
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-06990-8
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Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 3  
PCT-US02-09239-8  
; Sequence 8, Application PC/TUS0209239  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS953PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09239  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/278,650  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 09/950,082  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/950,083  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-09239-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 4  
PCT-US02-09135-8  
; Sequence 8, Application PC/TUS0209135  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS956PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09135  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/278,650  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 09/950,082  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/950,083  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-09135-8

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Db 1 ggggacttccc 12

RESULT 5  
PCT-US02-09105-8  
; Sequence 8, Application PC/TUS0209105  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS951PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09105  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/278,650  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 09/950,082  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/950,083  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 779  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-09105-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 6  
PCT-US02-09188-8  
; Sequence 8, Application PC/TUS0209188  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS952PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09188  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/278,650  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 09/950,082  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/950,083  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 1732  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-09188-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 7  
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; Sequence 8, Application PC/TUS0209257  
; GENERAL INFORMATION:



APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS957PCT  
CURRENT APPLICATION NUMBER: PCT/US02/09257  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/278,650  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: US 09/950,082  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US 09/950,083  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 994  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-09257-8

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Qy 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 8  
PCT-US02-09370-8  
Sequence 8, Application PC/TUS0209370  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS954PCT  
CURRENT APPLICATION NUMBER: PCT/US02/09370  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/278,650  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: US 09/950,082  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US 09/950,083  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 1834  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-09370-8

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Qy 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 9  
PCT-US02-09785-8  
Sequence 8, Application PC/TUS0209785  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS905PCT  
CURRENT APPLICATION NUMBER: PCT/US02/09785  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US 60/331,287  
PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/306,171  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/277,340  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 1130  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-09785-8

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Qy 1 ggggacttccc 12  
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Db 1 ggggacttccc 12

RESULT 10  
PCT-US02-09922-8  
Sequence 8, Application PC/TUS0209922  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS955PCT  
CURRENT APPLICATION NUMBER: PCT/US02/09922  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/278,650  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: US 09/950,082  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US 09/950,083  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 1117  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-09922-8

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Db 1 ggggacttccc 12

RESULT 11  
PCT-US02-17699-8  
Sequence 8, Application PC/TUS0217699  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc., et al.  
TITLE OF INVENTION: Secreted Proteins From Diabetes-Related Tissues  
FILE REFERENCE: PS737PCT  
CURRENT APPLICATION NUMBER: PCT/US02/17699  
CURRENT FILING DATE: 2002-06-05  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-17699-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
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DB 1 999gacttccc 12

RESULT 12  
PCT-US02-23214-30

; Sequence 30, Application PC/TUS0223214  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Keratinocyte Derived Interferon  
; FILE REFERENCE: PF482PCT3  
; CURRENT APPLICATION NUMBER: PCT/US02/23214  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 60/336,165  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 09/908,594  
; PRIOR FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-23214-30

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
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DB 1 999gacttccc 12

RESULT 13  
PCT-US02-25107-8

; Sequence 8, Application PC/TUS0225107  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: 13 Human Secreted Proteins  
; FILE REFERENCE: PS738PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/25107  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 60/311,085  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/325,209  
; PRIOR FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-25107-8

Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
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DB 1 999gacttccc 12

RESULT 14  
PCT-US02-21857-14

; Sequence 14, Application PC/TUS0221857  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: LP Mammalian Proteins: Related Reagents Field of the Invention  
; FILE REFERENCE: X-14499  
; CURRENT APPLICATION NUMBER: PCT/US02/21857  
; CURRENT FILING DATE: 2002-08-23  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
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; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
PCT-US02-21857-14

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Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
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DB 1 999gacttccc 12

RESULT 15  
US-09-852-659A-8

; Sequence 8, Application US/09852659A  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 28 Human Secreted Proteins  
; FILE REFERENCE: P2003P4  
; CURRENT APPLICATION NUMBER: US/09/852,659A  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/265,583  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/152,060  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: PCT/US98/04858  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/040,762  
; PRIOR FILING DATE: 1997-03-14  
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; PRIOR FILING DATE: 1997-03-14  
; PRIOR APPLICATION NUMBER: 60/050,934  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,100  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,357  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,189  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/057,765  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,368  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-852-659A-8

Query Match 100.0%; Score 12; DB 5; Length 12;  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Title: US-09-400-322-1  
Perfect score: 12  
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Scoring table: IDENTITY\_NUC  
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Searched: 1736436 seqs, 858457221 residues

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Maximum Match 100%  
Listing first 45 summaries

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- 24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	12	100.0	12	19	AAV59508
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4	12	100.0	12	19	AAV69608
5	12	100.0	12	20	AAZ32078
6	12	100.0	12	20	AAZ24808
7	12	100.0	12	20	AAZ09781
8	12	100.0	12	20	AAZ00407
9	12	100.0	12	20	AAZ00799

10	12	100.0	12	20	AAZ06216	Nuclear factor kap
11	12	100.0	12	20	AAZ97913	Nuclear factor kap
12	12	100.0	12	20	AAZ79008	Upstream primer fo
13	12	100.0	12	20	AAZ84930	Nuclear factor kap
14	12	100.0	12	20	AAZ37366	Nuclear factor kap
15	12	100.0	12	20	AAZ37448	Human NF-kappab pr
16	12	100.0	12	20	AAZ27308	Nuclear factor kap
17	12	100.0	12	20	AAZ30180	Nuclear factor kap
18	12	100.0	12	20	AAZ22208	Upstream primer fo
19	12	100.0	12	20	AAZ22108	Upstream primer fo
20	12	100.0	12	20	AAZ30314	Nucleotide sequenc
21	12	100.0	12	20	AAZ20409	Nuclear factor kap
22	12	100.0	12	20	AAZ16175	Nuclear factor-kB
23	12	100.0	12	20	AAZ04308	Nuclear factor kap
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26	12	100.0	12	21	AAZ02084	Nuclear factor kap
27	12	100.0	12	21	AAZ02236	Nuclear factor kap
28	12	100.0	12	21	AAZ22038	Nuclear factor kap
29	12	100.0	12	21	AAZ22313	Nuclear factor kap
30	12	100.0	12	21	AAZ22370	Nuclear factor kap
31	12	100.0	12	21	AAZ98770	Nuclear factor kap
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33	12	100.0	12	21	AAZ99815	Nuclear factor kap
34	12	100.0	12	21	AAZ16512	Nuclear factor kap
35	12	100.0	12	21	AAZ18431	Nuclear factor kap
36	12	100.0	12	21	AAZ66407	NF-kappab promoter
37	12	100.0	12	21	AAZ67628	Nuclear factor kap
38	12	100.0	12	21	AAZ68078	Nuclear factor kap
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#### ALIGNMENTS

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ID AAV34151 standard; DNA; 12 BP.  
AC AAV34151;  
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XX  
DT 02-FEB-1999 (first entry)  
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XX  
DE Upstream primer for nuclear factor kappa-B gene promoter.  
XX  
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
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XX  
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FN WO9839446-A2.  
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PD 11-SEP-1998.  
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PF 06-MAR-1998; 98WO-US04492.  
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PR 07-MAR-1997; 97US-0038621.  
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PR 07-MAR-1997; 97US-0040163.

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PR 07-MAR-1997; 97US-0040333.
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PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043315.
PR 11-APR-1997; 97US-0043368.
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PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
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PR 23-MAY-1997; 97US-0047502.
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PR 23-MAY-1997; 97US-0047583.
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PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
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PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.

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PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferlie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-609887/51.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Example 16; Page 226; 721pp; English.
XX
XX The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC (see AAV34154 for described uses). The genes can be used to generate
CC fusion proteins by linking to the gene to a sequence encoding human
CC immunoglobulin Fc portion (AAV34145) for increasing the stability of the
CC fused protein as compared to the secreted protein only. Genes encoding
CC the secreted proteins can be used for high-throughput assays for
CC biological activities. Expression of the genes can be driven by a range
CC of promoter active in eukaryotic cells. Primers AAV34151-V34152 are used
CC to amplify the nuclear factor kappa-B (NF-kB) gene promoter (AAV34153) to
CC generate a construct for identifying proteins involved in immune
CC responses.
XX
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;
SQ
Query Match 100.0%; Score 12; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 5,1e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ggggacttccc 12
| | | | | | | | | |
Db 1 ggggacttccc 12
RESULT 2
AAV59508
ID AAV59508 standard; DNA; 12 BP.
XX AAV59508;
AC
XX
XX 02-FEB-1999 (first entry)
DT
XX
XX Upstream primer for nuclear factor kappa-B gene promoter.
DE
XX

```

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN MO9839448-A2.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PE 06-MAR-1998; 98WO-US04493.  
 XX  
 PR 02-OCT-1997; 97US-0061060.  
 PR 07-MAR-1997; 97US-0038621.  
 PR 07-MAR-1997; 97US-0040161.  
 PR 07-MAR-1997; 97US-0040162.  
 PR 07-MAR-1997; 97US-0040163.  
 PR 07-MAR-1997; 97US-0040333.  
 PR 07-MAR-1997; 97US-0040334.  
 PR 07-MAR-1997; 97US-0040336.  
 PR 07-MAR-1997; 97US-0040626.  
 PR 11-APR-1997; 97US-0043311.  
 PR 11-APR-1997; 97US-0043312.  
 PR 11-APR-1997; 97US-0043313.  
 PR 11-APR-1997; 97US-0043314.  
 PR 11-APR-1997; 97US-0043568.  
 PR 11-APR-1997; 97US-0043569.  
 PR 11-APR-1997; 97US-0043576.  
 PR 11-APR-1997; 97US-0043578.  
 PR 11-APR-1997; 97US-0043580.  
 PR 11-APR-1997; 97US-0043669.  
 PR 11-APR-1997; 97US-0043670.  
 PR 11-APR-1997; 97US-0043671.  
 PR 11-APR-1997; 97US-0043672.  
 PR 11-APR-1997; 97US-0043674.  
 PR 23-MAY-1997; 97US-0047492.  
 PR 23-MAY-1997; 97US-0047500.  
 PR 23-MAY-1997; 97US-0047501.  
 PR 23-MAY-1997; 97US-0047502.  
 PR 23-MAY-1997; 97US-0047503.  
 PR 23-MAY-1997; 97US-0047581.  
 PR 23-MAY-1997; 97US-0047582.  
 PR 23-MAY-1997; 97US-0047583.  
 PR 23-MAY-1997; 97US-0047584.  
 PR 23-MAY-1997; 97US-0047585.  
 PR 23-MAY-1997; 97US-0047586.  
 PR 23-MAY-1997; 97US-0047587.  
 PR 23-MAY-1997; 97US-0047588.  
 PR 23-MAY-1997; 97US-0047589.  
 PR 23-MAY-1997; 97US-0047590.  
 PR 23-MAY-1997; 97US-0047592.  
 PR 23-MAY-1997; 97US-0047593.  
 PR 23-MAY-1997; 97US-0047594.  
 PR 23-MAY-1997; 97US-0047595.  
 PR 23-MAY-1997; 97US-0047596.  
 PR 23-MAY-1997; 97US-0047597.  
 PR 23-MAY-1997; 97US-0047598.  
 PR 23-MAY-1997; 97US-0047599.  
 PR 23-MAY-1997; 97US-0047600.  
 PR 23-MAY-1997; 97US-0047601.  
 PR 23-MAY-1997; 97US-0047612.  
 PR 23-MAY-1997; 97US-0047613.  
 PR 23-MAY-1997; 97US-0047614.  
 PR 23-MAY-1997; 97US-0047615.  
 PR 23-MAY-1997; 97US-0047617.  
 PR 23-MAY-1997; 97US-0047618.  
 PR 23-MAY-1997; 97US-0047632.

PR 23-MAY-1997; 97US-0047633.  
 PR 06-JUN-1997; 97US-0048964.  
 PR 13-JUN-1997; 97US-0048974.  
 PR 08-JUL-1997; 97US-0049610.  
 PR 16-JUL-1997; 97US-0051926.  
 PR 18-AUG-1997; 97US-0052874.  
 PR 22-AUG-1997; 97US-0055724.  
 PR 22-AUG-1997; 97US-0056630.  
 PR 22-AUG-1997; 97US-0056631.  
 PR 22-AUG-1997; 97US-0056632.  
 PR 22-AUG-1997; 97US-0056636.  
 PR 22-AUG-1997; 97US-0056637.  
 PR 22-AUG-1997; 97US-0056662.  
 PR 22-AUG-1997; 97US-0056664.  
 PR 22-AUG-1997; 97US-0056845.  
 PR 22-AUG-1997; 97US-0056862.  
 PR 22-AUG-1997; 97US-0056864.  
 PR 22-AUG-1997; 97US-0056872.  
 PR 22-AUG-1997; 97US-0056874.  
 PR 22-AUG-1997; 97US-0056875.  
 PR 22-AUG-1997; 97US-0056876.  
 PR 22-AUG-1997; 97US-0056877.  
 PR 22-AUG-1997; 97US-0056878.  
 PR 22-AUG-1997; 97US-0056879.  
 PR 22-AUG-1997; 97US-0056880.  
 PR 22-AUG-1997; 97US-0056881.  
 PR 22-AUG-1997; 97US-0056882.  
 PR 22-AUG-1997; 97US-0056884.  
 PR 22-AUG-1997; 97US-0056886.  
 PR 22-AUG-1997; 97US-0056887.  
 PR 22-AUG-1997; 97US-0056888.  
 PR 22-AUG-1997; 97US-0056889.  
 PR 22-AUG-1997; 97US-0056892.  
 PR 22-AUG-1997; 97US-0056893.  
 PR 22-AUG-1997; 97US-0056894.  
 PR 22-AUG-1997; 97US-0056903.  
 PR 22-AUG-1997; 97US-0056908.  
 PR 22-AUG-1997; 97US-0056909.  
 PR 22-AUG-1997; 97US-0056910.  
 PR 22-AUG-1997; 97US-0056911.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057659.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bedharik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
 PI Feng P, Ferrite AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 XX  
 DR WPI: 1998-506364/43.  
 XX  
 PT New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 XX  
 PS Example 16: Page 226; 721pp: English.  
 PS  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC polypeptides can be diagnosed by determining the amount of the new  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses). The genes can be used to generate  
 CC fusion proteins by linking to the gene to a sequence encoding human  
 CC immunoglobulin Fc portion (AAV59502) for increasing the stability of the  
 CC fused protein as compared to the secreted protein only. Genes encoding  
 CC the secreted proteins can be used for high-throughput assays for

CC biological activities. Expression of the genes can be driven by a range  
CC of promoter active in eukaryotic cells. Primers AAV59508-V59509 are used  
CC to amplify the nuclear factor kappa-B (NF-kB) gene promoter (AAV59510) to  
CC generate a construct for identifying proteins involved in immune  
CC responses.

XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
|||||  
DB 1 ggggacttccc 12

## RESULT 3

AAV34283 standard; DNA; 12 BP.

AC AAV34283;

DT 29-JAN-1999 (first entry)

DE Upstream primer for nuclear factor kappa-B gene promoter.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Synthetic.

OS Homo sapiens.

PN WO9840483-A2.

PD 17-SEP-1998.

PF 12-MAR-1998; 98WO-US04858.

PR 19-DEC-1997; 97US-0068368.

PR 14-MAR-1997; 97US-0040710.

PR 30-MAY-1997; 97US-0040762.

PR 30-MAY-1997; 97US-0048100.

PR 30-MAY-1997; 97US-0048189.

PR 30-MAY-1997; 97US-0048357.

PR 06-JUN-1997; 97US-0050934.

PR 05-SEP-1997; 97US-0048970.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Fertle AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

PI Li H, Li Y, Moore PA, Ruben CA, Ruben SM, Soppet DR;

PI Wei YF, Young PE, Zeng Z;

DR WPI; 1998-520811/44.

XX Isolated human poly(nucleotide(s) encoding secretory peptide(s) -  
PT used to develop products for the diagnosis and treatment of e.g.  
PT inflammation, cancers, CNS disorders or immune system disorders  
XX Example 16; Page 95; 201pp; English.  
XX The invention relates to 28 novel genes and their fragments (nucleic  
CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)  
CC which are useful for preventing, treating or ameliorating medical

CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 28  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAV34286 for described uses). The genes can be used to generate  
CC fusion proteins by linking to the gene to a sequence encoding human  
CC immunoglobulin Fc portion (AAV34277) for increasing the stability of the  
CC fused protein as compared to the secreted protein only. Genes encoding  
CC the secreted proteins can be used for high-throughput assays for  
CC biological activities. Expression of the genes can be driven by a range  
CC of promoter active in eukaryotic cells. Primers AAV34283-V34284 are used  
CC to amplify the nuclear factor kappa-B (NF-kB) gene promoter (AAV34285) to  
CC generate a construct for identifying proteins involved in immune  
CC responses.

XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
|||||  
DB 1 ggggacttccc 12

## RESULT 4

AAV69608 standard; DNA; 12 BP.

AC AAV69608;

DT 28-JAN-1999 (first entry)

DE Upstream primer for nuclear factor kappa-B gene promoter.

XX Secreted protein; gene therapy; protein therapy; diagnosis; treatment;  
KW central nervous system; CNS; immune system; cancer; trauma; liver;  
KW reproductive disorder; congenital malformation; degenerative disease;  
KW inflammatory disease; neoplasia; metabolic disorder; testis; placenta;  
KW brain; T cell; spleen; lung; heart; rhabdomyosarcoma; endocrine system;  
KW endocrinopathy; endocrine polyglandular syndrome; endocrinoma; sepsis;  
KW endocrine ophthalmopathy; osteoclastoma; bacterial infection; bone;  
KW primer; nuclear factor kappa-B; NF-kB; ds.

XX Synthetic.

OS Homo sapiens.

PN WO9845712-A2.

PD 15-OCT-1998.

PF 07-APR-1998; 98WO-US06801.

PR 30-MAY-1997; 97US-0048184.

PR 08-APR-1997; 97US-0042726.

PR 08-APR-1997; 97US-0042727.

PR 08-APR-1997; 97US-0042728.

PR 08-APR-1997; 97US-0042754.

PR 08-APR-1997; 97US-0042825.

PR 30-MAY-1997; 97US-0048068.

PR 30-MAY-1997; 97US-0048070.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Feng P, Ni J, Rosen CA, Ruben SM, Yu G;

PI WPI; 1998-594496/50.

XX New isolated human genes and secreted polypeptide(s) they encode -  
PT useful for the diagnosis and treatment of e.g. cancers, CNS



PT disorders, immune system disorders, inflammatory disease and  
 PT bacterial infections  
 XX  
 PS Example 16; Page 83; 142pp; English.  
 XX  
 CC The invention relates to 20 novel genes and their fragments (AAV69611 to  
 CC AAV69630) and corresponding secreted proteins (AAW83931 to AAW83950)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein of gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the  
 CC polynucleotides. Specific uses are based on which tissues they are most  
 CC highly expressed in (see AAV69611 for described uses). The genes can be  
 CC used to generate fusion proteins by linking to the gene, a sequence  
 CC encoding human immunoglobulin Fc portion (AAV69602) for increasing the  
 CC stability of the fused protein as compared to the secreted protein only.  
 CC Genes encoding the secreted proteins can be used for high-throughput  
 CC assays for biological activities. Expression of the genes can be driven  
 CC by a range of promoter active in eukaryotic cells. Primers  
 CC AAV69608-V69609 are used to amplify the nuclear factor kappa-B (NF-kB)  
 CC gene promoter (AAV69610) to generate a construct for identifying proteins  
 CC involved in immune responses.  
 CC  
 XX  
 SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match: 100.0%; Score 12; DB 19; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
 |||||  
 Db 1 999gacttccc 12

RESULT 5  
 AA232078  
 ID AA232078 standard; DNA; 12 BP.  
 AC AA232078;  
 XX  
 DT 10-JAN-2000 (first entry)  
 XX  
 DE Nuclear factor KB binding site.  
 XX  
 KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;  
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;  
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;  
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;  
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;  
 KW arterial-venous malformation; immune deficiency; ss.  
 XX  
 OS Homo sapiens.  
 PN WO9937660-A1.  
 PD 29-JUL-1999.  
 XX  
 PF 22-JAN-1999; 99WO-US01313.  
 XX  
 PR 23-JAN-1998; 98US-0072298.  
 PR 28-AUG-1998; 98US-0098539.  
 XX  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Irueja-Arispe L, Hastings GA, Ruben SM;  
 XX  
 DR WPI; 1999-590684/50.  
 XX  
 PT New isolated metalloprotease thrombospondin polypeptides, useful for  
 PT treating hyperproliferative disorders, cancers or autoimmune disorders

PT  
 XX  
 PS Example 19; Page 158; 457pp; English.  
 XX  
 CC AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human  
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2  
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of  
 CC angiogenesis both in vitro and in vivo. They can be used for treating  
 CC cancer and other disorders related to angiogenesis including abnormal  
 CC wound healing, inflammation, rheumatoid arthritis, psoriasis,  
 CC endometrial bleeding disorders, diabetic retinopathy, some forms of  
 CC macula degeneration, haemangiomas, and arterial-venous malformations.  
 CC They may be useful in treating deficiencies or disorders of the immune  
 CC system, by activating or inhibiting the proliferation, differentiation,  
 CC or mobilization (chemotaxis) of immune cells. The etiology of these  
 CC immune deficiencies or disorders may be genetic, somatic, such as  
 CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or  
 CC toxins), or infectious. They can also be used to treat inflammatory  
 CC conditions, both chronic and acute conditions. The products can also be  
 CC used for detection and diagnosis. AA232002 to AA232080, and AAY49503 to  
 CC AAY49511 represent sequences given in the exemplification of the present  
 CC invention.  
 CC  
 XX  
 SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match: 100.0%; Score 12; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
 |||||  
 Db 1 999gacttccc 12

RESULT 6  
 AA224808  
 ID AA224808 standard; DNA; 12 BP.  
 AC AA224808;  
 XX  
 DT 02-DEC-1999 (first entry)  
 XX  
 DE Nuclear factor kappa-B binding site sequence.  
 XX  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ss;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO9947540-A1.  
 PD 23-SEP-1999.  
 XX  
 PF 18-MAR-1999; 99WO-US05804.  
 XX  
 PR 19-MAR-1998; 98US-0078563.  
 PR 19-MAR-1998; 98US-0078566.  
 PR 19-MAR-1998; 98US-0078573.  
 PR 19-MAR-1998; 98US-0078574.  
 PR 19-MAR-1998; 98US-0078576.  
 PR 19-MAR-1998; 98US-0078577.  
 PR 19-MAR-1998; 98US-0078578.  
 PR 19-MAR-1998; 98US-0078579.  
 PR 19-MAR-1998; 98US-0078581.  
 PR 01-APR-1998; 98US-0080312.

PR 01-APR-1998; 9805-0080313.  
 PR 01-APR-1998; 9805-0080314.  
 XX  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;  
 PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW;  
 PI Olsen HS, Shi Y, Moore PA;  
 XX  
 DR WPI: 1999-562050/47.  
 XX  
 PT New isolated human genes, useful for diagnosis and treatment of e.g.  
 PT cancers, neurological disorders, immune diseases, inflammation or blood  
 PT disorders  
 XX  
 PS Example 16; Page 262; 484pp; English.  
 XX  
 CC The invention relates to 95 novel genes and their fragments (nucleic  
 CC acid sequences: AA224811-224907; amino acid sequences AA41308-Y41404)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 95  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AA224811 for described uses). The genes can be used to generate  
 CC fusion proteins by linking to the gene to a sequence encoding human  
 CC immunoglobulin Fc portion (AA224802) for increasing the stability of the  
 CC fused protein as compared to the secreted protein only. Genes encoding  
 CC the secreted proteins can be used for high-throughput assays for  
 CC biological activities. Expression of the genes can be driven by a range  
 CC of promoter active in eukaryotic cells. This sequence represents the  
 CC nuclear factor kappa-B (NF-kB) binding site sequence which is used to  
 CC generate a construct (AA224810) for identifying proteins involved in  
 CC immune responses.  
 XX  
 SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;  
 XX

Query Match 100.0%; Score 12; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
 |||||||  
 Db 1 999gacttccc 12

RESULT 7  
 AA209781  
 ID AA209781 standard; DNA; 12 BP.  
 XX  
 AC AA209781;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Nuclear factor kappaB binding site DNA motif.  
 XX  
 KW Secreted protein; human; gene therapy; diagnosis; treatment; cancer;  
 KW protein therapy; tumor; neurodegenerative disorder; blood disorder; AIDS;  
 KW developmental abnormality; leukemia; immune system; autoimmune disease;  
 KW hepatic disease; renal disease; inflammation; allergy; schizophrenia;  
 KW Alzheimer's disease; cognitive disorder; arthritis; infection; psoriasis;  
 KW transplant rejection; diabetes; asthma; sepsis; acne; metabolic disorder;  
 KW cardiovascular disorder; food additive; preservative; NF-kappaB;  
 KW nuclear factor kappaB; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9946289-A1.  
 XX  
 PD 16-SEP-1999.  
 XX

PF 11-MAR-1999; 99WO-0505721.  
 XX  
 PR 12-MAR-1998; 98US-0077686.  
 PR 12-MAR-1998; 98US-0077687.  
 PR 12-MAR-1998; 98US-0077696.  
 PR 12-MAR-1998; 98US-0077714.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ferrle AM, Rosen CA, Florence C, Young PE, Yu G, NI J;  
 PI WPI: 1999-551363/46.  
 XX  
 DR New isolated human genes, useful for diagnosis and treatment of, e.g.  
 DR cancers  
 XX  
 PT  
 PT  
 PS Example 16; Page 148; 306pp; English.  
 XX  
 CC This invention describes novel human genes and the secreted proteins they  
 CC encode. The polynucleotides and their corresponding secreted polypeptides  
 CC are useful for preventing, treating or ameliorating medical conditions  
 CC e.g. by protein or gene therapy. Also pathological conditions can be  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new polynucleotides.  
 CC Specific uses are described for each of the polynucleotides of the  
 CC invention, based on which tissues they are most highly expressed in, and  
 CC include developing products for the diagnosis or treatment of cancer,  
 CC tumors, neurodegenerative disorders, developmental abnormalities, blood  
 CC disorders, leukemias, diseases of the immune system, autoimmune diseases,  
 CC hepatic and renal disease, inflammation, allergies, Alzheimer's and  
 CC cognitive disorders, schizophrenia, arthritis, infections, AIDS,  
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,  
 CC cardiovascular disorders, and metabolic disorders. The polypeptides or  
 CC polynucleotides can also be used as food additives or preservatives. This  
 CC polypeptides are also useful for identifying their binding partners. This  
 CC sequence represents a nuclear factor kappaB (NF-kappaB) binding site  
 CC motif which is used for the construction of a NF-kappaB/SV40 promoter  
 CC construct which is used in the method of the invention.  
 XX  
 SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;  
 XX

Query Match 100.0%; Score 12; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
 |||||||  
 Db 1 999gacttccc 12

RESULT 8  
 AA200407  
 ID AA200407 standard; DNA; 12 BP.  
 XX  
 AC AA200407;  
 XX  
 DT 04-OCT-1999 (first entry)  
 XX  
 DE Human NF-kappaB binding site DNA motif.  
 XX  
 KW Secreted protein; human; treatment; diagnosis; therapy; cancer; tumor;  
 KW neurodegenerative disorder; developmental abnormality; blood disorder;  
 KW fetal deficiency; blood disorder; leukemia; immune system; inflammation;  
 KW autoimmune disease; hepatic disease; renal disease; allergy; restenosis;  
 KW ischemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;  
 KW cardiovascular disorder; wound healing; stroke; arthritis; obesity;  
 KW asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;  
 KW metabolic disorder; NF-kappaB; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9938881-A1.  
 XX

```
XX 05-AUG-1999.
PD
XX
PE 27-JAN-1999; 99WO-US01621.
XX
PR 30-JAN-1998; 98US-0073170.
PR 30-JAN-1998; 98US-0073159.
PR 30-JAN-1998; 98US-0073160.
PR 30-JAN-1998; 98US-0073161.
PR 30-JAN-1998; 98US-0073162.
PR 30-JAN-1998; 98US-0073164.
PR 30-JAN-1998; 98US-0073165.
PR 30-JAN-1998; 98US-0073167.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Carter KC, Endress GA, Feng P, Ferlie AM, Florence C;
PI Florence KA, Janat F, NI J, Rosen CA, Ruben SM;
PI Soppet DR, Young P, Yu G;
XX
XX WPI: 1999-469315/39.
DR
XX
PT New isolated human genes and the secreted polypeptides they encode
PT useful in, e.g. treatment of Alzheimer's
XX
XX
PS Example 16; Page 255; 393pp; English.
XX
CC This invention describes novel human genes and the secreted proteins they
CC encode. The polynucleotides and their corresponding secreted polypeptides
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 67 polynucleotides of the
CC invention, based on which tissues they are most highly expressed in, and
CC include developing products for the diagnosis or treatment of cancer,
CC tumours, neurodegenerative disorders, developmental abnormalities and
CC fetal deficiencies, blood disorders, leukemias, diseases of the immune
CC system, autoimmune diseases, hepatic and renal disease, inflammation,
CC allergies, ischemic shock, Alzheimer's and cognitive disorders,
CC schizophrenia, restenosis, cardiovascular disorders, wound healing,
CC stroke, arthritis, obesity, asthma, sepsis, acne, psoriasis, transplant
CC rejection, metabolic disorders, infections and AIDS. The polypeptides
CC are also useful for identifying their binding partners. This sequence
CC represents the human NF-kappab binding site DNA motif which is used to
CC describe the method of the invention.
XX
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other:
SQ
Query Match 100.0%; Score 12; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ggggacttccc 12
Db 1 ggggacttccc 12
IIIIIIIIII
RESULT 9
AAZ00799 standard; DNA; 12 BP.
ID AAZ00799;
AC AAZ00799;
XX
XX 11-OCT-1999 (first entry)
DE NF-kappab DNA binding site motif.
XX
XX Secreted protein: prevention; treatment; protein therapy; gene therapy;
KW diagnosis; cancer; tumour; neurodegenerative disorder; blood disorder;
KW developmental abnormality; fetal deficiency; leukemia; autoimmune; acne;
KW hepatic disease; renal disease; lymphoma; inflammation; allergy; asthma;
```

```
KW Alzheimer's disease; cognitive disorder; schizophrenia; obesity; sepsis;
KW osteoporosis; arthritis; infection; AIDS; connective tissue disorder;
KW transplant rejection; diabetes; psoriasis; cardiovascular disorder;
KW reproductive disorder; food additive; food preservative; human;
KW NF-kappab; nuclear factor Kappab; ss.
XX
XX Homo sapiens.
OS
XX WO9940100-A1.
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US02293.
XX
XX 09-FEB-1998; 98US-0074341.
PR 09-FEB-1998; 98US-0074037.
PR 09-FEB-1998; 98US-0074118.
PR 09-FEB-1998; 98US-0074141.
PR 09-FEB-1998; 98US-0074157.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Kyaw H, Lafleur DW, Moore PA, Rosen CA, Ruben SM;
PI Shi Y, Wei Y;
XX
XX WPI: 1999-479426/40.
DR
XX
PT New isolated human genes potentially useful for, e.g. developmental
PT abnormalities and fetal deficiencies
XX
XX
PS Example 16; Page 173; 263pp; English.
XX
CC This invention describes novel isolated human genes and the secreted
CC proteins they encode. The polynucleotides and their corresponding
CC secreted polypeptides are useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. Also pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for the
CC polynucleotides of the invention based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, neurodegenerative disorders, developmental
CC abnormalities and fetal deficiencies, blood disorders, leukemias,
CC diseases of the immune system, autoimmune diseases, hepatic and renal
CC disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive
CC disorders, schizophrenia, obesity, osteoporosis, arthritis, infections,
CC AIDS, connective tissue disorders, transplant rejection, diabetes,
CC asthma, sepsis, acne, psoriasis, cardiovascular disorders, and
CC reproductive disorders. The polypeptides or polynucleotides can also be
CC used as food additives or preservatives. The polypeptide are also useful
CC for identifying their binding partners. This sequence represents a DNA
CC binding motif from the nuclear factor Kappab (NF-kappab) which is used
CC to describe the method of the invention.
XX
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other:
SQ
Query Match 100.0%; Score 12; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ggggacttccc 12
Db 1 ggggacttccc 12
IIIIIIIIII
RESULT 10
AAZ06216
ID AAZ06216 standard; DNA; 12 BP.
AC AAZ06216;
XX
XX 30-SEP-1999 (first entry)
DE
```

```
XX DE Nuclear factor kappa-B binding site sequence.
XX DE
XX DE
XX DE Human: secreted protein; cancer; tumour; neurodegenerative disorder; leukemia;
XX DE diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
XX DE developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX DE immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;
XX DE inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX DE cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX DE osteoporosis; arthritis; testis; thyroiditis; thyroid; digestion;
XX DE endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO935158-A1.
XX PD 15-JUL-1999.
XX PF 06-JAN-1999; 99WO-US00108.
XX PR 07-JAN-1998; 98US-0070704.
XX PR 07-JAN-1998; 98US-0070657.
XX PR 07-JAN-1998; 98US-0070658.
XX PR 07-JAN-1998; 98US-0070692.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Brewer LA, Duan RD, Edner R, Lafleur DM, NI J;
XX PI Olsen HS, Rosen CA, Ruben SM, Soppet DR;
XX DR WPI: 1999-444190/37.
XX PT New isolated human genes and the secreted polypeptides they encode
XX PS
XX PS Example 16; Page 126; 227pp; English.
XX CC The invention relates to 36 novel genes and their fragments (nucleic
XX CC acid sequences: AA206219-Z06263; amino acid sequences AAY3386-Y38458)
XX CC which are useful for preventing, treating or ameliorating medical
XX CC conditions e.g. by protein or gene therapy. Also, pathological
XX CC conditions can be diagnosed by determining the amount of the new
XX CC polypeptides in a sample or by determining the presence of mutations in
XX CC the new polynucleotides. Specific uses are described for each of the 36
XX CC polynucleotides, based on which tissues they are most highly expressed in
XX CC (see AA206219 for described uses). The genes can be used to generate
XX CC fusion proteins by linking to the gene to a sequence encoding human
XX CC immunoglobulin Fc portion (AA206210) for increasing the stability of the
XX CC fused protein as compared to the secreted protein only. Genes encoding
XX CC the secreted proteins can be used for high-throughput assays for
XX CC biological activities. Expression of the genes can be driven by a range
XX CC of promoter active in eukaryotic cells. This sequence represents the
XX CC nuclear factor kappa-B (NF-kB) binding site sequence which is used to
XX CC generate a construct (AA206218) for identifying proteins involved in
XX CC immune responses.
XX SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other:
XX
XX Query Match 100.0%; Score 12; DB 20; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 5.1e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 999gacttcgcc 12
XX |111111111111
XX DB 1 999gacttcgcc 12
XX
XX RESULT 11
XX AAX97913
XX ID AAX97913 standard; DNA; 12 BP.
XX XX
XX AC AAX97913;
```

```
XX XX 17-SEP-1999 (first entry)
XX DT
XX DE Nuclear factor kappa-B binding site sequence.
XX DE
XX DE
XX DE Human: secreted protein; cancer; tumour; developmental abnormality;
XX DE foetal deficiency; blood disorder; immune system disorder; inflammation;
XX DE autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
XX DE schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
XX DE atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
XX DE digestive disorder; endocrine disorder; infection; AIDS; ss.
XX OS Homo sapiens.
XX OS
XX PN WO931117-A1.
XX PD 24-JUN-1999.
XX PF 17-DEC-1998; 98WO-US27059.
XX PR 19-DEC-1997; 97US-0068369.
XX PR 18-DEC-1997; 97US-0068006.
XX PR 18-DEC-1997; 97US-0068007.
XX PR 18-DEC-1997; 97US-0068008.
XX PR 18-DEC-1997; 97US-0068053.
XX PR 18-DEC-1997; 97US-0068054.
XX PR 18-DEC-1997; 97US-0068057.
XX PR 18-DEC-1997; 97US-0068064.
XX PR 18-DEC-1997; 97US-0070923.
XX PR 19-DEC-1997; 97US-0068169.
XX PR 19-DEC-1997; 97US-0068365.
XX PR 19-DEC-1997; 97US-0068367.
XX PR 19-DEC-1997; 97US-0068368.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Carter KC, Duan RD, Feng P, Ferrite AM, Florence C;
XX PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;
XX PI NI J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y;
XX PI Yu G;
XX DR WPI: 1999-418749/35.
XX PT New isolated human genes encoding secreted polypeptides
XX PS
XX PS Example 16; Page 247; 537pp; English.
XX CC AAX97916 to AAX98029 represent 110 isolated human secreted protein
XX CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by
XX CC the 110 human genes. The genes and their corresponding secreted
XX CC polypeptides are useful for preventing, treating or ameliorating medical
XX CC conditions, e.g. by protein or gene therapy. Also pathological conditions
XX CC can be diagnosed by determining the amount of the new polypeptides in a
XX CC sample or by determining the presence of mutations in the new genes.
XX CC Specific uses are described for each of the 110 genes, based on which
XX CC tissues they are most highly expressed in, and include developing
XX CC products for the diagnosis or treatment of cancer, tumours, developmental
XX CC abnormalities and foetal deficiencies, blood disorders, diseases of the
XX CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's
XX CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,
XX CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular
XX CC disorders, kidney disorders, digestive/endocrine disorders, infections
XX CC and AIDS. The polypeptides are also useful for identifying their binding
XX CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are
XX CC used in the exemplification of the present invention.
XX SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other:
XX
XX Query Match 100.0%; Score 12; DB 20; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 5.1e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 999gacttccc 12  
 |||||  
 Db 1 999gacttccc 12

RESULT 12  
 AAX79008  
 ID AAX79008 standard; DNA: 12 BP.  
 XX  
 AC AAX79008;  
 XX  
 DT 17-AUG-1999 (first entry)  
 XX  
 DE Upstream primer for nuclear factor kappa-B gene promoter.  
 XX

KM Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal; ss;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Synthetic.  
 OS Homo sapiens.

XX  
 XX MO9919339-A1.

PN 22-APR-1999.  
 PD  
 XX  
 XX 08-OCT-1998; 98WO-US21142.

PF 09-OCT-1997; 97US-0071498.  
 PR 09-OCT-1997; 97US-0061463.  
 PR 09-OCT-1997; 97US-0061527.  
 PR 09-OCT-1997; 97US-0061529.  
 PR 09-OCT-1997; 97US-0061532.  
 PR 09-OCT-1997; 97US-0061536.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Brewer LA, Duan R, Ebner R, Ferris AM, Florence C;  
 PI Florence KA, Greene JM, Olsen HS, Rosen CA, Ruben SM;  
 PI Young PE, Yu G;

XX WPI; 1999-277587/23.

XX New isolated human genes and the secreted polypeptides they encode

PS Example 16; Page 138; 226pp; English.

CC The invention relates to 53 novel genes and their fragments (nucleic  
 CC acid sequences: AAX79011-X79064; amino acid sequences AAY14411-Y14464)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 53  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAX79011 for described uses). The genes can be used to generate  
 CC fusion proteins by linking to the gene to a sequence encoding human  
 CC immunoglobulin Fc portion (AAX79002) for increasing the stability of the  
 CC fused protein as compared to the secreted protein only. Genes encoding  
 CC the secreted proteins can be used for high-throughput assays for  
 CC biological activities. Expression of the genes can be driven by a range  
 CC of promoter active in eukaryotic cells. This sequence represents the  
 CC nuclear factor kappa-B (NF-kB) binding site sequence which is used to  
 CC generate a construct (AAX79010) for identifying proteins involved in  
 CC immune responses.

XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5,1e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
 |||||  
 Db 1 999gacttccc 12

RESULT 13  
 AAX84930  
 ID AAX84930 standard; DNA: 12 BP.  
 XX  
 AC AAX84930;  
 XX  
 DT 30-JUL-1999 (first entry)  
 XX  
 DE Nuclear factor kappa-B binding site sequence.  
 XX

KM Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Synthetic.  
 OS Homo sapiens.

XX  
 XX MO9924836-A1.

PN 20-MAY-1999.

PD 04-NOV-1998; 98WO-US23435.

PF 17-NOV-1997; 97US-0066100.  
 PR 07-NOV-1997; 97US-0064900.  
 PR 07-NOV-1997; 97US-0064908.  
 PR 07-NOV-1997; 97US-0064911.  
 PR 07-NOV-1997; 97US-0064912.  
 PR 07-NOV-1997; 97US-0064983.  
 PR 07-NOV-1997; 97US-0064984.  
 PR 07-NOV-1997; 97US-0064985.  
 PR 07-NOV-1997; 97US-0064987.  
 PR 07-NOV-1997; 97US-0064988.  
 PR 17-NOV-1997; 97US-0066090.  
 PR 17-NOV-1997; 97US-0066094.  
 PR 17-NOV-1997; 97US-0066095.  
 PR 17-NOV-1997; 97US-0066089.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;  
 PI Kraw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruden SM, Shi Y, Soppet DR, Wei Y;

XX WPI; 1999-337740/28.

XX New human secreted proteins and coding sequences useful for treating  
 XX disorders of the immune system and hyperproliferative disorders

PS Example 16; Page 259; 507pp; English.

CC The invention relates to 125 novel genes and their fragments (nucleic  
 CC acid sequences: AAX84933-X85057; amino acid sequences AAY27567-Y27933)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 125

CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX84933 for described uses). The genes can be used to generate  
CC fusion proteins by linking to the gene to a sequence encoding human  
CC immunoglobulin Fc portion (AAX84924) for increasing the stability of the  
CC fused protein as compared to the secreted protein only. Genes encoding  
CC biological activities. Expression of the genes can be driven by a range  
CC of promoter active in eukaryotic cells. This sequence represents the  
CC nuclear factor kappa-B (NF-kB) binding site sequence which is used to  
CC generate a construct (AAX84932) for identifying proteins involved in  
CC immune responses.

XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

SO

Query Match 100.0%; Score 12; DB 20; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gagcttcgcc 12  
|||||  
Db 1 999gagcttcgcc 12

RESULT 14  
AAX37366  
ID AAX37366 standard; DNA; 12 BP.

XX AAX37366;  
XX  
DT 06-JUL-1999 (first entry)

XX Human NF-kappaB promoter element PCR primer 1.

XX  
XX  
XX Human: secreted protein; prevention; treatment; protein therapy; AIDS;  
KW gene therapy; diagnosis; cancer; tumor; neurodegenerative disorder;  
KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;  
KW leukemia; immune system disorder; autoimmune disease; hepatic disease;  
KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;  
KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;  
KW arthritis; psoriasis; digestive; endocrine; infection; promoter;  
XX PCR primer; NF-kappaB; ss.

XX  
OS Synthetic.  
OS Homo sapiens.

XX  
XX  
XX WO9909155-A1.  
XX  
XX 25-FEB-1999.

XX  
XX  
XX 18-AUG-1998; 98WO-US17044.  
XX  
XX  
XX 16-JUN-1998; 98US-0092956.  
XX  
XX 15-JUL-1998; 98US-0092956.  
XX  
XX 19-AUG-1997; 97US-0056368.  
XX  
XX 19-AUG-1997; 97US-0056369.  
XX  
XX 19-AUG-1997; 97US-0056535.  
XX  
XX 19-AUG-1997; 97US-0056555.  
XX  
XX 19-AUG-1997; 97US-0056556.  
XX  
XX 19-AUG-1997; 97US-0056628.  
XX  
XX 19-AUG-1997; 97US-0056629.  
XX  
XX 19-AUG-1997; 97US-0056726.  
XX  
XX 19-AUG-1997; 97US-0056728.

XX  
XX (HUMA-) HUMAN GENOME SCI INC.

XX  
XX Brewer LA, Duan R, Ebner R, Endress GA, Feng P,  
PI Florence C, Florence KA, Komatsoulis GA, Latleur DW;  
PI Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR;  
XX Young PE;  
XX WPI: 1999-190160/16.  
XX

PT New isolated human genes and the secreted polypeptides they encode  
PT - useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders

XX  
XX  
XX Example 16; Page 164; 280pp; English.

XX  
XX This invention describes novel isolated human secreted proteins and  
CC their encoding nucleic acid sequences. The products of the invention  
CC are useful for preventing, treating or ameliorating medical conditions  
CC e.g. by protein or gene therapy. Also pathological conditions can be  
CC diagnosed by determining the presence or amount of expression of  
CC the new polypeptides in a sample or by determining the presence or  
CC absence of mutations in the new polynucleotides. Specific uses are  
CC described for each of the 70 PNs, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis  
CC or treatment of cancer, tumours, neurodegenerative disorders,  
CC developmental abnormalities and foetal deficiencies, blood disorders,  
CC leukemias, diseases of the immune system, autoimmune diseases, hepatic  
CC and renal disease, lymphomas, inflammation, allergies, asthma, sepsis,  
CC diabetes, Alzheimer's and cognitive disorders, schizophrenia,  
CC osteoporosis, arthritis, psoriasis, digestive/endocrine disorders,  
CC infections and AIDS. The human secreted proteins of the invention are  
CC represented in AAY07744-X07850 and the encoding nucleic acids are  
XX represented in AAX37369-X37441.

XX  
XX  
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

SO

Query Match 100.0%; Score 12; DB 20; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gagcttcgcc 12  
|||||  
Db 1 999gagcttcgcc 12

RESULT 15  
AAX37448  
ID AAX37448 standard; DNA; 12 BP.

XX AAX37448;  
XX  
XX  
XX 06-JUL-1999 (first entry)

XX  
XX  
XX NF-kappaB promoter element PCR primer 1.

XX  
XX  
XX Human: secreted protein; prevention; treatment; protein therapy; AIDS;  
KW gene therapy; diagnosis; cancer; tumor; neurodegenerative disorder;  
KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;  
KW immune system disorder; autoimmune disease; hepatic disease; lymphoma;  
KW renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia;  
KW cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder;  
KW pulmonary disorder; transplant rejection; osteoclast; osteoporosis;  
KW arthritis; malignancy; digestive; endocrine; infection; promoter;  
XX NF-kappaB; PCR primer; ss.

XX  
XX  
XX Synthetic.  
XX  
XX WO9918208-A1.  
XX  
XX 15-APR-1999.

XX  
XX  
XX 01-OCT-1998; 98WO-US20775.  
XX  
XX  
XX 02-OCT-1997; 97US-0060884.  
XX  
XX 02-OCT-1997; 97US-0060833.  
XX  
XX 02-OCT-1997; 97US-0060836.  
XX  
XX 02-OCT-1997; 97US-0060837.  
XX  
XX 02-OCT-1997; 97US-0060838.  
XX  
XX 02-OCT-1997; 97US-0060839.  
XX  
XX 02-OCT-1997; 97US-0060843.  
XX  
XX 02-OCT-1997; 97US-0060862.

PR 02-OCT-1997; 97US-0060866.  
PR 02-OCT-1997; 97US-0060874.  
XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Carter KC, Duan DR, Endress GA, Feng P, Ferlie AM;  
PI Florence KA, Greene JM, Janat F, Lafleur DW, Ni J;  
PI Rosen CA, Ruben SM, Shi Y, Young P, Yu G;  
XX

DR WPI; 1999-264022/22.

XX New isolated human genes and the secreted polypeptides they encode  
PT

PS Example 16; Page 198; 368pp; English.

XX This invention describes novel isolated human genes and the secreted  
CC proteins they encode. The products of the invention are useful for  
CC preventing, treating or ameliorating medical conditions, e.g. by protein  
CC or gene therapy. Also pathological conditions can be diagnosed by  
CC determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 101 Polynucleotides, based  
CC on which tissues they are most highly expressed in, and include  
CC developing products for the diagnosis or treatment of cancer, tumours,  
CC neurodegenerative disorders, developmental abnormalities and fetal  
CC deficiencies, blood disorders, leukemias, diseases of the immune system,  
CC autoimmune diseases, hepatic and renal disease, lymphomas, inflammation,  
CC allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate  
CC disease, skeletal or cardiac muscle disorders, pulmonary disorders,  
CC transplant rejection, disorders involving osteoclasts such as  
CC osteoporosis, arthritis or malignancies, digestive/endocrine disorders,  
CC infections and AIDS. The human secreted proteins of the invention are  
CC represented in AAY07852-Y07993 and the encoding nucleic acids are  
CC represented in AAX7451-X37552.

XX SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 12; DB 20; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
| | | | | | | | | | | | | |  
Pb 1 999gacttccc 12

Search completed: September 22, 2002, 13:26:07  
Job time: 4253 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 11:53:49 ; Search time 45.5 Seconds  
(without alignments)  
64.782 Million cell updates/sec

Title: US-09-400-322-1  
Perfect score: 12  
Sequence: 1 ggggacttccc 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/lna/5A-COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A-COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B-COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	US-08-723-052-1	Sequence 1, Appli
2	12	100.0	12	US-08-106-182-21	Sequence 21, Appli
3	12	100.0	12	US-09-274-625-1	Sequence 1, Appli
4	12	100.0	12	US-09-095-485-2	Sequence 2, Appli
5	12	100.0	12	US-09-274-624-1	Sequence 1, Appli
6	12	100.0	12	US-09-400-322-1	Sequence 1, Appli
7	12	100.0	12	US-09-227-357-8	Sequence 8, Appli
8	12	100.0	12	US-09-724-594-1	Sequence 1, Appli
9	12	100.0	12	US-08-632-275-3	Sequence 3, Appli
10	12	100.0	12	US-09-097-929-3	Sequence 1, Appli
11	12	100.0	12	US-08-664-173A-1	Sequence 1, Appli
12	12	100.0	12	US-08-797-696-1	Sequence 2, Appli
13	12	100.0	12	US-09-037-712-2	Sequence 1, Appli
14	12	100.0	12	US-08-157-808-1	Sequence 1, Appli
15	12	100.0	12	US-09-157-808-2	Sequence 2, Appli
16	12	100.0	12	PCT-US94-05659-15	Sequence 15, Appli
17	12	100.0	12	US-09-106-182-22	Sequence 9, Appli
18	12	100.0	12	US-09-227-357-9	Sequence 24, Appli
19	12	100.0	12	US-09-106-182-24	Sequence 10, Appli
20	12	100.0	12	US-08-227-357-10	Sequence 70, Appli
21	12	100.0	12	US-08-253-155A-70	Sequence 4, Appli
22	12	100.0	12	US-09-386-493-4	Sequence 1, Appli
23	12	100.0	12	US-07-971-092-1	Sequence 1, Appli
24	12	100.0	12	5198342-1	Sequence 8, Appli
25	12	100.0	12	US-09-228-986-8	Sequence 1, Appli
26	12	100.0	12	US-08-560-398-1	Sequence 1, Appli
27	12	100.0	12	US-09-083-351-1	Sequence 1, Appli

c 28	12	100.0	3946	4	US-09-083-352-1	Sequence 1, Appli
c 29	12	100.0	9511	1	US-07-925-695-6	Sequence 6, Appli
c 30	12	100.0	9511	1	US-07-925-695-7	Sequence 9, Appli
c 31	11	91.7	11	1	US-07-768-437-9	Sequence 2, Appli
c 32	11	91.7	13	2	US-08-353-476-2	Sequence 3, Appli
c 33	11	91.7	13	2	US-08-353-476-3	Sequence 16, Appli
c 34	11	91.7	13	3	US-08-646-789A-16	Sequence 49, Appli
c 35	11	91.7	13	3	US-08-646-789A-49	Sequence 36, Appli
c 36	11	91.7	14	3	US-08-646-789A-36	Sequence 92, Appli
c 37	11	91.7	14	3	US-08-646-789A-92	Sequence 4, Appli
c 38	11	91.7	15	2	US-08-353-476-4	Sequence 8, Appli
c 39	11	91.7	17	1	US-07-768-437-8	Sequence 3, Appli
c 40	11	91.7	20	2	US-08-850-993-3	Sequence 6, Appli
c 41	11	91.7	21	4	US-09-021-247-6	Sequence 1, Appli
c 42	11	91.7	23	3	US-08-353-765-1	Sequence 7, Appli
c 43	11	91.7	24	5	PCT-US92-10792-7	Sequence 4, Appli
c 44	11	91.7	25	4	US-08-930-500-4	Sequence 5, Appli
c 45	11	91.7	25	4	US-08-930-500-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-723-052-1  
; Sequence 1, Application US/08723052  
; Patent No. 5922757  
; GENERAL INFORMATION:  
; APPLICANT: Chojkier, Mario  
; APPLICANT: Carlson, Dennis  
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,052  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Christopher J.  
; REGISTRATION NUMBER: 40,179  
; REFERENCE/DOCKET NUMBER: UCSD-02424  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/705-8410  
; TELEFAX: 415/397-8338  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-723-052-1

Query Match 100.0%; Score 12; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
DB 1 ggggacttccc 12

RESULT 2  
US-09-106-182-21  
; Sequence 21, Application US/09106182  
; Patent No. 6046035  
; GENERAL INFORMATION:  
; APPLICANT: Sui, Yangu  
; APPLICANT: Ruben, Steve  
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc  
; STREET: 9410 Key West Ave  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/106,182  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/051,053  
; FILING DATE: 30-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF385  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-106-182-21  
Query Match 100.0%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 999gacttccc 12  
DB 1 GGGGACTTCCC 12

COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/274,625  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/274,624  
; FILING DATE: 23-MAR-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: UCSD-03683  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/705-8410  
; TELEFAX: 415/397-8338  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-274-625-1  
Query Match 100.0%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 999gacttccc 12  
DB 1 GGGGACTTCCC 12

RESULT 4  
US-09-095-485-2  
; Sequence 2, Application US/09095485  
; Patent No. 6127176  
; GENERAL INFORMATION:  
; APPLICANT: Stark, George R.  
; APPLICANT: Li, Xiaoxia  
; TITLE OF INVENTION: Mutant Cell Lines Unresponsive to  
; TITLE OF INVENTION: Interleukin 1  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter & Griswold LLP  
; STREET: 1400 McDonald Investment Center, 800 Superior  
; STREET: Avenue  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: United States  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,485  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Docherty, Pamela A.  
; REGISTRATION NUMBER: 40,591  
; REFERENCE/DOCKET NUMBER: 23114/04028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 622 8416  
; TELEFAX: (216) 241 0816  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-095-485-2

Query Match 100.0%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggggacttccc 12  
|||||  
Db 1 GGGGACTTCCC 12

RESULT 5  
US-09-274-624-1  
Sequence 1, Application US/09274624  
Patent No. 6147123

GENERAL INFORMATION:  
APPLICANT: Choikier, Mario  
TITLE OF INVENTION: TREATMENT AND PREVENTION OF  
TITLE OF INVENTION: HEPATIC DISORDERS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/274,624  
FILING DATE: 23-MAR-1999  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: UCSD-03683  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/705-8410  
TELEFAX: 415/397-8338  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-274-624-1

Query Match 100.0%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggggacttccc 12  
|||||  
Db 1 GGGGACTTCCC 12

RESULT 6  
US-09-400-322-1  
Sequence 1, Application US/09400322  
Patent No. 6218437

GENERAL INFORMATION:  
APPLICANT: Choikier, Mario  
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS  
FILE REFERENCE: UCSD-03831  
CURRENT APPLICATION NUMBER: US/09/400,322  
CURRENT FILING DATE: 1999-09-21  
EARLIER APPLICATION NUMBER: 08/723,052  
EARLIER FILING DATE: 1996-09-30  
EARLIER APPLICATION NUMBER: 09/274,624  
EARLIER FILING DATE: 1999-03-23  
EARLIER APPLICATION NUMBER: 09/274,625  
EARLIER FILING DATE: 1999-03-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 1  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-400-322-1

Query Match 100.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggggacttccc 12  
|||||  
Db 1 ggggacttccc 12

RESULT 7  
US-09-227-357-8  
Sequence 8, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919

EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-227-357-8

Query Match 100.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
Db 1 ggggacttccc 12

RESULT 8  
US-09-724-594-1  
Sequence 1, Application US/09724594  
Patent No. 6348493  
GENERAL INFORMATION:  
APPLICANT: Choklier, Mario  
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS  
FILE REFERENCE: UCSD-03831  
CURRENT APPLICATION NUMBER: US/09/724,594  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/400,322  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/274,624  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/274,625  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 12

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-724-594-1

Query Match 100.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
Db 1 ggggacttccc 12

RESULT 9  
US-08-632-275-3  
Sequence 3, Application US/08632275  
Patent No. 5840277  
GENERAL INFORMATION:  
APPLICANT: Ghio, Andrew J.  
TITLE OF INVENTION: Treatment of Chronic Pulmonary  
TITLE OF INVENTION: Inflammation  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: 1211 East Morehead Street  
CITY: Charlotte  
STATE: No. 5840277th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/632,275  
FILING DATE: 15-APR-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/413,699  
FILING DATE: 30-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Lipscomb, Ernest B.  
REGISTRATION NUMBER: 24,733  
REFERENCE/DOCKET NUMBER: 8751-5-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 704-331-6000  
TELEFAX: 704-334-2014  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FRAGMENT TYPE: linear  
US-08-632-275-3

Query Match 100.0%; Score 12; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
Db 7 GGGGACTTCCC 18

RESULT 10

US-09-097-929-3  
; Sequence 3, Application US/09097929  
; Patent No. 6024940  
; GENERAL INFORMATION:  
; APPLICANT: Ghio, Andrew J.  
; APPLICANT: Kennedy, Thomas P.  
; TITLE OF INVENTION: Treatment of Chronic Pulmonary  
; TITLE OF INVENTION: Inflammation  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson  
; STREET: 1211 East Morehead Street  
; CITY: Charlotte  
; STATE: No. 6024940th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,929  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,275  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lipscomb, Ernest B.  
; REGISTRATION NUMBER: 24,733  
; REFERENCE/DOCKET NUMBER: 8751-5-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 704-331-6000  
; TELEFAX: 704-334-2014  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FRAGMENT TYPE: linear  
; US-09-097-929-3

Query Match 100.0%; Score 12; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
|||||  
DB 7 GGGGACTTCCC 18

RESULT 11  
US-08-664-173A-1  
; Sequence 1, Application US/08664173A  
; Patent No. 6090938  
; GENERAL INFORMATION:  
; APPLICANT: Wakschull, Eric  
; APPLICANT: Mackin, William M.  
; APPLICANT: Zimmerman, Janet  
; TITLE OF INVENTION: Receptor for Underivatized, Aqueous  
; TITLE OF INVENTION: Soluble B (1-3)-Glucan  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,173A  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/637,934  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carroll, Alice O.  
; REGISTRATION NUMBER: 33,542  
; REFERENCE/DOCKET NUMBER: ABY95-06A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-664-173A-1

Query Match 100.0%; Score 12; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggacttccc 12  
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DB 7 GGGGACTTCCC 18

RESULT 12  
US-08-797-696-1  
; Sequence 1, Application US/08797696  
; Patent No. 6110692  
; GENERAL INFORMATION:  
; APPLICANT: Wakschull, Eric  
; APPLICANT: Mackin, William M.  
; APPLICANT: Zimmerman, Janet  
; TITLE OF INVENTION: Receptor for Underivatized, Aqueous  
; TITLE OF INVENTION: Soluble B (1-3)-Glucan  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,696  
; FILING DATE: 31-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/664,173  
; FILING DATE: 14-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/637,934  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carroll, Alice O.  
; REGISTRATION NUMBER: 33,542

REFERENCE/DOCKET NUMBER: ABY95-06A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-797-696-1

Query Match 100.0%; Score 12; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
|||||  
DB 7 GGGGACTTCCC 18

RESULT 13  
US-09-037-712-2  
Sequence 2, Application US/09037712  
Patent No. 6123943

GENERAL INFORMATION:  
APPLICANT: BABA, Masanori  
APPLICANT: ONO, Minoru  
TITLE OF INVENTION: NF-B ACTIVITY INHIBITOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sughrue, Lion, Macpeak & Seas, PLLC  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037-3202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,712  
FILING DATE: 10-MAR-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: JAHNS, Kristina M.  
REGISTRATION NUMBER: 41,092  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-037-712-2

Query Match 100.0%; Score 12; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
|||||  
DB 7 GGGGACTTCCC 18

RESULT 14

US-09-157-808-1  
Sequence 1, Application US/09157808  
Patent No. 6312896

GENERAL INFORMATION:  
APPLICANT: Heroux, Jeffrey A  
APPLICANT: Kibbey, Maura C  
APPLICANT: Kenten, John H  
TITLE OF INVENTION: Assays for Measuring Nucleic Acid Binding Proteins and  
FILE REFERENCE: P09100US  
CURRENT APPLICATION NUMBER: US/09/157,808  
CURRENT FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1

LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc-difference  
LOCATION: (1)..(8)  
OTHER INFORMATION: Nucleotides are linked by phosphorothioate linkages

NAME/KEY: misc-difference  
LOCATION: (16)..(22)  
OTHER INFORMATION: Nucleotides are linked by phosphorothioate linkages  
FEATURE:  
NAME/KEY: misc-difference  
LOCATION: (1)

OTHER INFORMATION: 5'-labeled with ruthenium tris-bipyridyl  
FEATURE:  
NAME/KEY: misc-difference  
LOCATION: (22)  
OTHER INFORMATION: 3'-labeled with biotin  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
OTHER INFORMATION: sequence containing a consensus sequence for human  
US-09-157-808-1

Query Match 100.0%; Score 12; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
|||||  
DB 7 ggggacttccc 18

RESULT 15  
US-09-157-808-2/c  
Sequence 2, Application US/09157808  
Patent No. 6312896

GENERAL INFORMATION:  
APPLICANT: Heroux, Jeffrey A  
APPLICANT: Kibbey, Maura C  
APPLICANT: Kenten, John H  
TITLE OF INVENTION: Assays for Measuring Nucleic Acid Binding Proteins and  
FILE REFERENCE: P09100US  
CURRENT APPLICATION NUMBER: US/09/157,808  
CURRENT FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2

LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
OTHER INFORMATION: sequence containing consensus sequence for human  
OTHER INFORMATION: NFKB

US-09-157-808-2

Query Match 100.0%; Score 12; DB 4; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 16 GGGGACTTCCC 5

Search completed: September 22, 2002, 13:22:12  
 Job time: 5303 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 11:30:20 ; Search time 1872.1 Seconds  
(without alignments)  
134.137 Million cell updates/sec

Title: US-09-400-322-1  
12  
Perfect score: 1  
Sequence: 1 ggggacttccc 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_in:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_inv:\*  
33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query Match Length DB ID Description

1	1	100.0	12	6	AR098339	Sequence 1 from patent US 6075027.	12 bp	DNA	linear	PAT 14-FEB-2001
2	2	100.0	12	6	AR111721					
3	3	100.0	12	6	AR141741					
4	4	100.0	12	6	AR146394					
5	5	100.0	22	6	AR059258					
6	6	100.0	22	6	AR107990					
7	7	100.0	22	6	AR176711					
8	8	100.0	22	6	AR176712					
9	9	100.0	22	6	AX019403					
10	10	100.0	22	6	AX195273					
11	11	100.0	22	6	AX299025					
12	12	100.0	116	6	AX189780					
13	13	100.0	116	6	AX189781					
14	14	100.0	199	6	AX189782					
15	15	100.0	268	9	HUMRRTH					
16	16	100.0	275	10	RATSR72R					
17	17	100.0	277	9	HS4399934					
18	18	100.0	300	9	HS21E8R					
19	19	100.0	336	11	G17247					
20	20	100.0	354	9	HS285094					
21	21	100.0	372	9	AB071192S1					
22	22	100.0	372	9	HSCD89EX3					
23	23	100.0	372	9	HS285093					
24	24	100.0	380	4	SS297397					
25	25	100.0	387	6	AX302813					
26	26	100.0	395	11	HS291WE5					
27	27	100.0	396	6	AX198652					
28	28	100.0	396	6	AX209187					
29	29	100.0	398	11	HS27S2F5					
30	30	100.0	417	10	AF104150					
31	31	100.0	423	6	I76242					
32	32	100.0	471	9	AF305868					
33	33	100.0	492	8	AF461579					
34	34	100.0	540	9	D87856					
35	35	100.0	576	9	D87854					
36	36	100.0	576	9	S82919					
37	37	100.0	585	9	HSIGAFCR4					
38	38	100.0	608	9	HSU43677					
39	39	100.0	613	9	HS4335319					
40	40	100.0	618	9	D87860					
41	41	100.0	654	9	D87858					
42	42	100.0	679	8	AF461581					
43	43	100.0	679	8	AF461582					
44	44	100.0	725	9	HS4330092					
45	45	100.0	754	9	D87857					

## ALIGNMENTS

RESULT 1  
LOCUS AR098339 12 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 1 from patent US 6075027.  
ACCESSION AR098339  
VERSION AR098339.1 GI:12807596  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chojkier, M. and Carson, D.  
TITLE Treatment and prevention of hepatic disorders  
JOURNAL Patent: US 6075027-A 1 13-JUN-2000;  
FEATURES  
SOURCE Location/Qualifiers  
1..12  
BASE COUNT 1 a 4 c 4 g 3 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
Db 1 GGGGACTTCCC 12

RESULT 2  
LOCUS AR11721 12 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 2 from patent US 6127176.  
ACCESSION AR11721  
VERSION AR11721.1 GI:12828569  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Stark,G.R. and Li,X.  
TITLE Mutant cell lines unresponsive to interleukin 1  
JOURNAL Patent: US 6127176-A 2 03-OCT-2000;  
FEATURES Location/Qualifiers  
1..12  
source /organism="unknown"

BASE COUNT 1 a 4 c 4 g 3 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
Db 1 GGGGACTTCCC 12

RESULT 3  
LOCUS AR141741 12 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6147123.  
ACCESSION AR141741  
VERSION AR141741.1 GI:15101257  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chojkier,M. and Carson,D.  
TITLE Treatment and prevention of hepatic disorders  
JOURNAL Patent: US 6147123-A 1 14-NOV-2000;  
FEATURES Location/Qualifiers  
1..12  
source /organism="unknown"

BASE COUNT 1 a 4 c 4 g 3 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
Db 1 GGGGACTTCCC 12

RESULT 4  
LOCUS AR146394 12 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6218437.  
ACCESSION AR146394  
VERSION AR146394.1 GI:15109583

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chojkier,M.  
TITLE Treatment and prevention of hepatic disorders  
JOURNAL Patent: US 6218437-A 1 17-APR-2001;  
FEATURES Location/Qualifiers  
1..12  
source /organism="unknown"

BASE COUNT 1 a 4 c 4 g 3 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
Db 1 GGGGACTTCCC 12

RESULT 5  
LOCUS AR059258 22 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5840277.  
ACCESSION AR059258  
VERSION AR059258.1 GI:5985708  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Ghio,A.J. and Kennedy,T.P.  
TITLE Treatment of chronic pulmonary inflammation  
JOURNAL Patent: US 5840277-A 3 24-NOV-1998;  
FEATURES Location/Qualifiers  
1..22  
source /organism="unknown"

BASE COUNT 4 a 5 c 8 g 5 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 999gacttccc 12  
Db 7 GGGGACTTCCC 18

RESULT 6  
LOCUS AR107990 22 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 1 from patent US 6110692.  
ACCESSION AR107990  
VERSION AR107990.1 GI:12823477  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Wakschull,E., Macklin,W.M. and Zimmerman,J.  
TITLE Receptor for underivatized aqueous soluble .beta.(1-3)-glucan  
JOURNAL Patent: US 6110692-A 1 29-AUG-2000;  
FEATURES Location/Qualifiers  
1..22  
source /organism="unknown"

BASE COUNT 4 a 5 c 8 g 5 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
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 DB 7 GGGGACTTCCC 18

## RESULT 7

LOCUS AR176711 22 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 1 from patent US 6312896.  
 ACCESSION AR176711  
 VERSION AR176711.1 GI:17919066  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Heroux,J.A., Kibbey,M.C. and Kenten,J.H.  
 TITLE Assays for measuring nucleic acid binding proteins and enzyme activities  
 JOURNAL Patent: US 6312896-A 1 06-NOV-2001;  
 FEATURES Location/Qualifiers  
 source 1..22

BASE COUNT 4 a 5 c 8 g 5 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
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 DB 7 GGGGACTTCCC 18

## RESULT 8

LOCUS AR176712/c 22 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 2 from patent US 6312896.  
 ACCESSION AR176712  
 VERSION AR176712.1 GI:17919067  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Heroux,J.A., Kibbey,M.C. and Kenten,J.H.  
 TITLE Assays for measuring nucleic acid binding proteins and enzyme activities  
 JOURNAL Patent: US 6312896-A 2 06-NOV-2001;  
 FEATURES Location/Qualifiers  
 source 1..22

BASE COUNT 5 a 8 c 5 g 4 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
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 DB 16 GGGGACTTCCC 5

## RESULT 9

LOCUS AX019403 22 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 19 from Patent W09940187.  
 ACCESSION AX019403  
 VERSION AX019403.1 GI:10043373  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Abken,H.  
 TITLE Nucleic acids provided for modulating cellular activation  
 JOURNAL Patent: WO 9940187-A 19 12-AUG-1999;  
 FEATURES Location/Qualifiers  
 source 1..22

BASE COUNT 4 a 5 c 8 g 5 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
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 DB 7 GGGGACTTCCC 18

## RESULT 10

LOCUS AX195273 22 bp DNA linear PAT 28-AUG-2001  
 DEFINITION Sequence 9 from Patent W00151671.  
 ACCESSION AX195273  
 VERSION AX195273.1 GI:15385824  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS McCarthy,J. and Cordell,B.  
 TITLE Methods for identifying inhibitors of neuronal degeneration  
 JOURNAL Patent: WO 0151671-A 9 19-JUL-2001;  
 FEATURES Location/Qualifiers  
 source 1..22

BASE COUNT 4 a 5 c 8 g 5 t  
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 999gacttccc 12  
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 DB 7 GGGGACTTCCC 18

## RESULT 11

LOCUS AX299025 22 bp DNA linear PAT 26-NOV-2001  
 DEFINITION Sequence 7 from Patent W00183713.  
 ACCESSION AX299025  
 VERSION AX299025.1 GI:17129015  
 KEYWORDS

SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (sites)  
AUTHORS Robbins, P.D., Lu, L. and Giannoukakis, N.  
TITLE The use of tolerogenic dendritic cells for enhancing tolerogenicity in a host and methods for making the same  
JOURNAL Patent: WO 0183713-A 7 08-NOV-2001;  
UNIV PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)  
FEATURES location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Synthesized nucleotide sequence"  
BASE COUNT 4 a 5 c 8 g 5 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
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Db 7 GGGGACTTTCCC 18

RESULT 12  
AX189780 116 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 11 from Patent WO0148187.  
ACCESSION AX189780  
VERSION AX189780.1 GI:15143151  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Webster, K.A.  
TITLE A molecular switch for regulating mammalian gene expression  
JOURNAL Patent: WO 0148187-A 11 05-JUL-2001;  
The University of Miami (US)  
FEATURES location/Qualifiers  
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/organism="synthetic construct"  
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/note="Oligonucleotide"  
BASE COUNT 22 a 35 c 37 g 22 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 116;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
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Db 23 GGGGACTTTCCC 34

RESULT 13  
AX189781 116 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 12 from Patent WO0148187.  
ACCESSION AX189781  
VERSION AX189781.1 GI:15143152  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Webster, K.A.  
TITLE A molecular switch for regulating mammalian gene expression

JOURNAL Patent: WO 0148187-A 12 05-JUL-2001;  
The University of Miami (US)  
FEATURES location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"  
BASE COUNT 22 a 35 c 31 g 28 t  
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 116;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggacttccc 12  
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Db 23 GGGGACTTTCCC 34

RESULT 14  
AX189782 199 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 13 from Patent WO0148187.  
ACCESSION AX189782  
VERSION AX189782.1 GI:15143153  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 199)  
AUTHORS Webster, K.A.  
TITLE A molecular switch for regulating mammalian gene expression  
JOURNAL Patent: WO 0148187-A 13 05-JUL-2001;  
The University of Miami (US)  
FEATURES location/Qualifiers  
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ACCESSION M29212  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 268)  
AUTHORS Gold, H.A., Topper, J.N., Clayton, D.A. and Craft, J.  
TITLE The RNA processing enzyme RNase P is identical to the 7th RNP and related to RNase P  
JOURNAL Science 245, 1377-1380 (1989)  
MEDLINE 89388247  
FEATURES location/Qualifiers  
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